

## REMARKS

Claims 6-9, 26, 27 and 32-34 are pending in this application. Claim 34 is amended herein to clarify and more particularly define the invention. No new matter is added by this amendment. In light of the following amendments and remarks, applicants respectfully request reconsideration of this application and allowance of the claims to issue.

### **I. Rejection under 35 U.S.C. § 112**

A. The Action states that claims 6-9, 26, 27 and 32-34 stand rejected under 35 U.S.C. § 112, first paragraph, for allegedly failing to comply with the written description requirement.

Claim 6 as presented herein encompasses a specific genus of nucleic acid sequences encoding peptides immunochemically reactive with antibodies to the Epstein Barr Virus (EBV) VCA-p18 or VCA-p40 proteins, comprising an epitope of the VCA-p18 or VCA-p40 protein, encoded within the EBV open reading frames BFRF3 and BdRF1, respectively and wherein said antibodies are antibodies having the same reactivity with VCA-p18 as antibodies produced by the hybridomas deposited at the European Collection of Animal Cell Cultures under deposit numbers 93020413 or 93020412 or antibodies having the same reactivity with VCA-p40 as antibodies produced by the hybridoma deposited at the European Collection of Animal Cell Cultures under deposit number 93020414.

In claim 6, the nucleic acid sequences encode peptides comprising an epitope of the VCA-p18 or VCA-p40 protein. The peptides encoded by the nucleic acid sequences of claim 6 are further defined by their immunoreactivity with hybridoma-derived antibodies to VCA-p18 and VCA-p40 defined as European Collection of Animal Cell Cultures deposit numbers 93020413 or 93020412 (VCA-p18) or deposit number 93020414 (VCA-p40). As one of skill in the art would recognize, hybridoma derived antibodies are monoclonal. One of skill in the art further recognizes that monoclonal antibodies are specific to a single epitope and that all of the antibodies produced from a single hybridoma are identical. Therefore, contrary to the arguments in the Office Action,

these antibodies are not heterogeneous and, thus, are sufficient to define the genus of nucleic acid sequences encompassed by claim 6.

Furthermore, the specification demonstrates actual reduction to practice of the nucleic acids of claim 6 and in particular, provides several examples of peptides comprising epitopes of this invention (e.g., SEQ ID NOs:2, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21 and 22; see pages 7-13 for description of peptides and fragments of this invention and Examples 4 and 5, Figures 4-6 and Table 1) that are reactive with the EBV VCA-p18 or VCA-p40 monoclonal antibodies of claim 6 and also provides examples of nucleic acid sequences encoding such peptides (e.g., SEQ ID NO:1, SEQ ID NO:3). Accordingly, one of skill in the art would recognize that applicants were in possession of the nucleic acid sequences of claim 6 at the time the present application was filed, as evidenced by the large numbers of representative species disclosed in the specification.

Therefore, applicants respectfully submit that all of the members of the genus of nucleic acids of claim 6 are adequately defined both structurally and functionally, leading one of ordinary skill in the art to the reasonable conclusion that applicants were in possession of the invention of claim 6 at the time this application was filed.

Claims 7 and 8 as presented herein respectively encompass a specific genus of nucleic acid sequences comprising the nucleotide sequence or a subsequence of SEQ ID NO:1, wherein the subsequence encodes a peptide that comprises an epitope that is immunochemically reactive with antibodies to EBV VCA-p19 protein (claim 7), and a specific genus of nucleic acid sequences comprising the nucleotide sequence or a subsequence of SEQ ID NO:3, wherein the subsequence encodes a peptide that comprises an epitope that is immunochemically reactive with antibodies to EBV VCA-p40 protein (claim 8).

In both claims 7 and 8, the subsequence is defined as encoding a peptide comprising an epitope. It would be readily recognized by one of skill in the art that applicants were in

possession of the genus of nucleic acid sequences of claims 7 and 8 at the time the application was filed because the specification provides several examples of peptides comprising epitopes of this invention (e.g., SEQ ID NOs: 2, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21 and 22; see pages 7-13 for description of peptides and fragments of this invention and Examples 4 and 5, Figures 4-6 and Table 1) that are reactive with the EBV VCA-p18 or VCA-p40 antibodies of this invention and also provides examples of nucleic acid sequences encoding such peptides (e.g., SEQ ID NO:1, SEQ ID NO:3). Thus, one of skill in the art would recognize that applicants were in possession of the nucleotide sequences and subsequences of claims 7 and 8 at the time the present application was filed, as evidenced by the large numbers of representative species disclosed in the specification.

In particular, all of the members of the genus of the nucleotide sequences of claims 7 and 8 could be readily identified by one of ordinary skill in the art on the basis of the disclosure of the nucleotide sequences of SEQ ID NO:1 or SEQ ID NO:3. Such a genus is not overly broad, considering that every member must be a subsequence of a disclosed sequence (SEQ ID NO:1 or SEQ ID NO:3), thereby defining the members of the genus structurally AND every member of the genus must also meet the functional requirement of encoding an EBV peptide comprising an epitope that is immunochemically reactive with antibodies to the EBV VCA-p18 protein or the EBV VCA-p40 protein. Thus, all of the members of the genus of nucleic acids of claims 7 and 8 are adequately defined both structurally and functionally, leading one of ordinary skill in the art to the reasonable conclusion that applicants were in possession of the invention of claims 7 and 8 at the time this application was filed.

Claims 9, 26 and 27 depend from claims 6, 7 and 8, respectively, and recite a vector molecule comprising the nucleic acid molecule of each respective independent claim. Because the nucleic acid sequences of claims 6, 7 and 8 are adequately described in the specification, the vectors of these claims are adequately described as well.

With regard to claims 32-33, the specification presents data that demonstrate that the inventors produced more than 330 12 mers of VCA-p40 and more than 160 12 mers of VCA-p18 as described in Examples 4 and 5 and as shown in Figures 4-6 and in Table 1 of the specification, thereby adequately describing the genus of 12 contiguous amino acids as set forth in these claims.. Specifically, Example 4 describes the production of a full set of peptides with a length of 12 amino acids and an overlap of 11 amino acids of the amino acid sequences of both ORFs BFRF3 (VCA-p18) and BDRF1 (VCA-p40) (page 30). These peptides were assayed for immunoreactivity with EBV-specific antibodies (Example 4, page 31 and Example 5, page 33) and results of these assays are shown for the VCA-p18 peptides in Figures 4 and 5 and for the VCA-p40 peptides in Figure 6. Specifically, Figure 6 shows immunoreactivity results of almost 340 peptides of VCA-p40 and Figures 4 and 5 show such results for more than 160 peptides of VCA-p18. Thus, one of skill in the art would reasonably conclude that the peptides of claims 32 and 33 are adequately supported in the specification

Further, claim 34 as presented herein recites an isolated nucleic acid sequence encoding the amino acid sequence of SEQ ID NO:5 or SEQ ID NO:6 or a combination of both, wherein said amino acid sequence is immunochemically reactive with antibodies to the Epstein-Barr Virus VCA-p18 protein. Thus, claim 34 recites a nucleic acid sequence encoding the specific amino acid sequences of SEQ ID NO: 5 and/or SEQ ID NO:6, which are disclosed in the specification at least on page 9, second paragraph. Thus, the nucleic acid sequences of claim 34 are adequately supported in the specification.

Thus, at least for the reasons set forth above, applicants believe that this rejection has been overcome and its withdrawal and allowance of the pending claims are respectfully requested.

**B.** The Action states that claims 6-9, 26, 27 and 32-34 stand rejected under 35 U.S.C. § 112, first paragraph, for allegedly failing to comply with the enablement requirement. Specifically, the Action states that to the extent that the claimed sequences are not adequately



described in the instant disclosure, claims 6-9, 26, 27 and 32-34 are also rejected under 35 U.S.C. § 112, first paragraph, as allegedly containing subject matter which was not described in the specification in such a way as to enable one skilled in the art to make and/or use the invention.

As discussed above, the subject matter of claims 6-9, 26, 27 and 32-34 is adequately described in the present specification. The specification not only adequately discloses the full genus of nucleic acid sequences of this invention, but also provides detailed teachings of how to make and use these nucleic acid sequences. See, in particular, the Examples set forth on pages 22-26, wherein numerous working examples are provided of the production and testing of numerous peptides of this invention. Thus, applicants respectfully submit that the present invention is adequately enabled and applicants thereby respectfully request withdrawal of this rejection.

## **II. Rejection under 35 U.S.C. § 102(b)**

A. The Action states that claims 6-9, 26, 27 and 32-34 stand rejected under 35 U.S.C. § 102(b) as allegedly anticipated by Laux et al. (*EMBO J.* 7:769-774 (1988)). Specifically, the Action states that Laux et al. teaches a nucleic acid sequence comprising instant SEQ ID NO:1 which encodes at least 12 contiguous amino acids of EBV VCA-p18 (the amino acid sequence SEQ ID NO:5). The Action further states that Laux et al. teaches a nucleic acid sequence comprising a sequence that shares 98.8% homology with instant SEQ ID NO:3 (subsequence thereof), which encodes 12 contiguous amino acids of an EBV VCA-40. On this basis, the Action concludes that Laux et al. anticipates the instant claims. Applicants respectfully disagree and traverse this rejection.

Specifically, applicants have performed multiple alignments comparing both the nucleotide and amino acid sequences of the present invention with those of Figure 2 of Laux et al. (NCBI Accession No. Y00835.1) and the sequence homology asserted in the Action to be present was not found (See enclosed Alignments 1-6). Accordingly, applicants respectfully submit that Laux et al. fails to disclose the nucleotide sequences of SEQ ID NO:1, or SEQ ID

NO:3 or any subsequences thereof encoding 12 contiguous amino acids, as claimed herein. If the Examiner maintains this rejection, it is respectfully requested that the Examiner specifically point out what portion of the sequences of Laux et al. have homology with the sequences of the present invention. Otherwise, applicants respectfully request that this rejection be withdrawn.

**B.** The Action states that claims 6-9, 26, 27 and 32-34 stand rejected under 35 U.S.C. § 102(b) as allegedly anticipated by Bankier et al. (*Mol. Biol. Med.* 1:425-445 (1983)). Specifically, the Action states that Bankier et al. teaches a nucleic acid sequence comprising instant SEQ ID NO:1, which encodes at least 12 contiguous amino acids of EBV VCA-p18 (the amino acid sequence SEQ ID NO:5). The Action further states that Bankier et al. teaches a nucleic acid sequence comprising a sequence that shares 98.8% homology with instant SEQ ID NO:3 (subsequence thereof), which encodes 12 contiguous amino acids of an EBV VCA-40. On this basis, the Action concludes that Bankier et al. anticipates the instant claims. Applicants respectfully disagree and traverse this rejection.

Specifically, applicants have performed multiple alignments comparing both the nucleotide and amino acid sequences of the present invention with those of Figure 2 of Bankier et al. and the sequence homology asserted in the Action to be present was not found (See enclosed Alignments 7-38). Accordingly, applicants respectfully submit that Bankier et al. fails to disclose the nucleotide sequences of SEQ ID NO:1, or SEQ ID NO:3 or any subsequences thereof encoding 12 contiguous amino acids as claimed herein. If the Examiner maintains this rejection, it is respectfully requested that the Examiner specifically point out what portion of the sequences of Bankier et al. have homology with the sequences of the present invention. Otherwise, applicants respectfully request that this rejection be withdrawn.

The points and concerns raised in the outstanding Office Action having been addressed in full, it is respectfully submitted that all of the claims of this application are in condition for allowance, which action is respectfully requested. Should the Examiner have any remaining

concerns, the Examiner is invited and encouraged to contact the undersigned attorney directly by telephone in order to expedite the prosecution of this application to allowance.

The Commissioner is authorized to charge Deposit Account No. 50-0220 in the amount of \$120.00 as fee for a one-month extension of time. This amount is believed to be correct. However, the Commissioner is authorized to charge any deficiency or credit any overpayment to Deposit Account No. 50-0220.

Respectfully submitted,



Mary L. Miller  
Registration No. 39,303

**Customer No. 20792**

Myers Bigel Sibley & Sajovec, P.A.  
P. O. Box 37428  
Raleigh, North Carolina 27627  
Telephone: (919) 854-1400  
Facsimile: (919) 854-1401

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Tracy Wallace

9310-13DVCTDV SEQ ID NO 1.xdna x Laux et al. EBV terminal gene.xdna => DNA Parallel

DNA sequence 538 bp catgatggcagc ... aaacagtagccc linear

DNA sequence 2227 bp gcagtgtgtgaa ... aaaaaaaaaa linear

Method: Blocks (Martinez)  
Layout: Standard  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Translation: Off

Alignment 1. Comparison of nucleotide sequence  
of SEQ ID NO:1 with the nucleotide sequence of  
Fig. 2 of Laux et al.

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1 gcagtgtgtgaagattgtcacagctgctggtttggagaaaacgggggtgggcggtgatca 60
   .               20               .               40               .               60
-----
61 gggagaacaattccccggggacacctgcacgagaccctgggctctcaggaactccgccc 120
   .               80               .               100              .               120
-----
121 aggtcttgccaattgggggtgatcctgtagcgccgcgggtttcagcatcacagggttattttg 180
   .               140              .               160              .               180
-----
181 cctgaagcttgctggggcgtaaataccctctcgccctgttttctcagagagcatttcaggcc 240
   .               200              .               220              .               240
-----
241 ggttttgcagtcgctgctgcagctatggggtcacctagaaatggtgccaatgggcgcgggt 300
   .               260              .               280              .               300
-----
301 cccctagccccggcggggatccggatgggtacgatggcggaacaactcccaatatcca 360
   .               320              .               340              .               360
-----
361 tctgcttctggctcttcttggaacacccccacccacccaacgatgaggaacgtgaatct 420
   .               380              .               400              .               420
-----
421 aatgaagagccccacccgcttatgaggaccatattggggcaatggcgaccgtcactcg 480
   .               440              .               460              .               480
-----
481 gactatcaaccactaggaacccaagatcaaagtctgtacttgggattgcaacacgacggg 540
   .               500              .               520              .               540
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541 aatgacgggctccctccccctccctactctccacgggatgactcatctcaacacatatac 600
   .               560              .               580              .               600

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 601 gaagaagcgggcagaggaagtatgaatccagtatgcctgcctgtaattgttgccgacctac 660  
                                 620                                640                                660  
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661 ctcttttggctggcggctattgccgcctcgtgtttcacggcctcagttagtaccgttgtg 720  
                                 680                                700                                720  
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721 accgccaccggcttggccctctcacttctactcttggcagcagtgccagctcatatgcc 780  
                                 740                                760                                780  
 -----

781 gctgcacaaaggaaactgctgacaccggtgacagtgttactgcggttgctactttcttt 840  
                                 800                                820                                840  
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841 gcaatttgcctaacatggaggattgaggaccaccttttaattctcttctgtttgcattg 900  
                                 860                                880                                900  
 -----

901 ctggccgcagctggcggactacaaggcatttacgttcttggtgatgcttgctcctgata 960  
                                 920                                940                                960  
 -----

961 ctagcgtacagaaggagatggcgccgtttgactgtttgtggcgcatcatgtttttggca 1020  
                                 980                                1000                                1020  
 -----

1021 tgtgtacttgtcctcatcgctcgacgctgttttgcagctgagtcacctccttggagctgta 1080  
                                 1040                                1060                                1080  
 -----

1                   catg----- 4  
                   ||||  
 1081 actgtggtttccatgacgctgctgctactggctttcgctcctctggtctctctcgccaggg 1140  
                                 1100                                1120                                1140  
 -----

1141 ggcctaggtactcttgggtgcagcccttttaacattggcagcagctctggcactgctagcg 1200  
                                 1160                                1180                                1200  
 -----

1201 tcaactgattttgggcacacttaacttgactacaatgttccttctcatgctcctatggaca 1260  
                                 1220                                1240                                1260  
 -----

1261 cttgtggttctcctgatttgcctcttcgtgctcttcatgtccactgagcaagatccttctg 1320  
                                 1280                                1300                                1320  
 -----

1321 gcaagactgttcctatatgctctcgcaactcttgttgctagcctccgcgctaatacgtgggt 1380  
                                 1340                                1360                                1380  
 -----

1381 ggcagtatTTTTgcaaacaacttcaagagtttaagcagcactgaattttatacccaatttg 1440  
 . 1400 . 1420 . 1440

1441 ttctgcatgttattactgattgtcgctggcatactcttcattcttgctatcctgaccgaa 1500  
 . 1460 . 1480 . 1500

1501 tggggcagtggaatatagaacatacgggtccagtttttatgtgcctcgggtggcctgctcacc 1560  
 . 1520 . 1540 . 1560

1561 atggtagccggcgctgtgtggctgacggtgatgtctaacacgcttttgtctgcctggatt 1620  
 . 1580 . 1600 . 1620

1621 cttacagcaggattcctgattttcctcattggcctttgccctctttggggtcattagatgc 1680  
 . 1640 . 1660 . 1680

1681 tgccgctactgctgctactactgccttacactggaaagtgaggagcgccaccgacccca 1740  
 . 1700 . 1720 . 1740

```

5 -----atggca 10
      |||||
1741 tatcgcaacactgtataaagaatgccaccagatcgctgccacttccacagcaatggca 1800
      .      1760      .      1780      .      1800
      20      .      40      .      60      .
11 cgccggctgccaagcccaccctccaggggaggctggaggcggattttccagacagtccc 70
   ||
1801 cg===== 1802

```

80                      .                      100                      .                      120                      .  
71 ctgcttcctaataattcaagagctgaaccagaataatctccccaatgatgttttctgggag 130

140 160 180  
131 gctcaaagaagttacctggtat-tt-ct--gac--atcccagttctgctacgaag-agta 183  
1803 =====gatgcctggcgcttttgctatgaattatccaagaaacccacggagcaggg 1852  
1820 1840

184 cg----tgcagag----- 192  
| | | | |  
1853 caacattgcagggctctgttcacgcgatggctcgtcatctggctctcctgtgtgacccctc 1912  
1860 . 1880 . 1900 .

193 -----gacttttgg-----g 202  
 |||||  
 1913 actttgtacagacttttggcaatgggagcacattccccccgcctttggggcaccacacggg 1972  
 1920 . 1940 . 1960 .

203 gtgcctcggcgcgaacgcgccatagacaagaggcgagagccagtgtggctggggctggt 262  
 |||||  
 1973 qtgc=====t 1977

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      280              300              320
263 gctcatgcacaccttggcgggtcatccgccacccccgtccagcaggctcaggccgccgca 322
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1978 ccccttggaaca=ctt=atgtttcaagcagctcacctat=ggta==ctcaggc===== 2025
    1980              2000              2020
      340              360              380
223 tccgctgggaccggggccttggcatcatcagcgccgtccacggccgtagcccagtc-cgc 381
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2026 =====acgggtcg=cccctccgagtgaccagtcacct 2055
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      400              420
382 gacccccctctgtttcttcatctattagc-----agcctccggggccgca 425
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2056 tccagactatgcatacactgaatttagcctgatattgtccccctagcc=ccggggcc==== 2110
    2060              2080              2100
      440              460              480
426 cttcggggggcgactgccgcgcctccgcccgcagccgctcgataccgggtcaggtggcg 485
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2111 =====cagc=cctcctcagaaaactctgcatgg==agaagctg 2145
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    2120              2140
      500              520
486 ggggacaaccccacgacaccgccccacgcggggcacgtaagaaacagtagccc----- 538
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
2146 gacgtgaacctc=ccccccagacctgtgtgtgtgta=tttacaacactacaataaaccca 2203
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
    2160              2180              2200

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2204 atgtgcaaaaaaaaaaaaaaaaaaaaaa 2227
    2220

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% Identity = 7.0 (174/2484)

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9310-13DVCTDV SEQ ID NO 3.xdna x Laux et al. EBV terminal gene.xdna => DNA Parallel

DNA sequence 1038 bp atgctatcaggt ... cgcgtggcttga linear

DNA sequence 2227 bp gcagtgtgtgaa ... aaaaaaaaaaaa linear

Method: Blocks (Martinez)  
Layout: Standard  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Translation: Off

Alignment 2. Comparison of nucleotide sequence  
of SEQ ID NO:3 with the nucleotide sequence of  
Fig. 2 of Laux et al.

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1 -----atgctatca 9
1 gcagtgtgtgaagattgtcacagctgctggtttggagaaaacgggggtgggcgggtgatca 60
      20      40      60
10 ggtaacgcaggagaa-ggag-caacagcctgcggaggttcggc----- 50
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
61 gggagaacaattccccggggacacctgcacgagaccctgggctctcaggaactccgccc 120
      80      100      120
51 -----cgccgcgggcccaggacctcatcagcgtcccc 81
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
121 aggtcttgccaattgggggtgatcctgtagcgcgcgg===tttcagcatca===== 168
      140      160
82 cgcaacacctttatgacactgcttcagaccaacctggacaacaaaccgccgaggcagacc 141
=====

      160      180      200
142 ccgctaccctacgcggccccgctgcccccttttcccaccaggcaatagccaccgcgcct 201
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
169 =====caggttattttgcc= 182
      180      220
202 tcttacgggtcctggggc-----cg 220
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
183 t=gaagcttgctggggcgtaaatccctctcgccttggtttctcagagagcatttcaggccg 241
      200      220      240
221 g-----a 222
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
242 gttttgcagtcgctgctgcagctatgggggtccctagaaatggtgccaatgggcgcgggtc 301
      260      280      300
223 gcgggtcgcggcgccggcggtactttacctccccaggaggttactacgccgggcccgcg 282
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
302 cccctagccccggc===== 315

      300      320
283 ggccggggaccggggtgccttcttggcgatggacgctcacacctac----- 327
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
316 ===ggggatccggatgggta===cgatgg=cggaacaactcccaatatccatctgct 366
      320      340      360
328 -----cacccccaccc----- 338
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
367 tctggctcttctgggaacacccccacccccaccgaacgatgaggaacgtgaatctaataa 426
      380      400      420

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427 gagccccaccgccttatgaggaccatattggggcaatggcgaccgtcactcggactat 486
      .               .               .               .
      440               460               480
-----
487 caaccactaggaaccaagatcaaagtctgtacttgggattgcaacacgacgggaatgac 546
      .               .               .               .
      500               520               540
340
339 -----acacccccctccggcctac----- 357
      | ||||| |||
547 gggctccctcccccctcc==ctactctccacgggatgactcatctcaacacatatagaa 603
      .               .               .               .
      560               580               600
-----
604 gaagcgggcagaggaagtatgaatccagtatgcctgcctgtaattggtgcgcctacctc 663
      .               .               .               .
      620               640               660
360
358 -tttggt-----tgccg----- 369
      ||||| |||
664 ttttggtggcggctattgcccgcctcgtgtttcacggcctcagttagtaccgttgtgacc 723
      .               .               .               .
      680               700               720
-----
724 gccaccggcttggccctctcacttctactcttggcagcagtggccagctcatatgccgct 783
      .               .               .               .
      740               760               780
-----
784 gcacaaaggaaactgctgacaccggtgacagtgttactgcggttgctcactttctttgca 843
      .               .               .               .
      800               820               840
-----
844 atttgcctaacatggaggattgaggaccaccttttaattctcttctgtttgcattgctg 903
      .               .               .               .
      860               880               900
-----
904 gccgcagctggcggactacaaggcatttacgttctggtgatgcttgtgctcctgatacta 963
      .               .               .               .
      920               940               960
-----
964 gcgtacagaaggagatggcgccgtttgactgtttgtggcggcatcatgtttttggcatgt 1023
      .               .               .               .
      980               1000              1020
-----
1024 gtacttgtcctcatcgtcgacgctgttttgacgtgagtcacctccttggagctgtaact 1083
      .               .               .               .
      1040              1060              1080
-----
1084 gtggtttccatgacgctgctgctactggctttcgtcctctggctctcttcgccagggggc 1143
      .               .               .               .
      1100              1120              1140
-----
1144 ctaggtactcttgggtgcagcccttttaacattggcagcagctctggcactgctagcgtca 1203
      .               .               .               .
      1160              1180              1200

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370 -----ggcctctttggccccctccaccgtgc 396

397 ct-----ccttac----- 404

405 -----tacggattcccacttgcgggcagactacgtcc 436

440 . 460 . 480 .  
437 ccgctccctcgcgatccaacaagcggaaaagagaccccgaggaggatgaagaaggcgggg 496

500 520 540  
497 ggctattcccggggaggacgccacctctaccgcaaggacatagcgggcctctccaaga 556

560 . 580 . 600 .  
557 gtgtgaatgagttacagcacacgctacaggccctgcgccgggagacgctgtcctacggcc 616

123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 1100 1101 1102 1103 1104 1105 1106 1107 1108 1109 1110 1111 1112 1113 1114 1115 1116 1

```
% Identity = 11.7 (323/2749)
```

///

9310-13DVCTDV SEQ ID NO 2.xprt x Laux et al. EBV terminal gene.xprt => Protein Alignment

Protein sequence 177 aa MARRLPKPTLQG ... DTAPRGARKKQ\*

Protein sequence 498 aa MGSLEMVPMGAG ... ERPPTPYRNTV\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 3.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:1 (SEQ ID NO:2) with the amino acid sequence encoded by the nucleotide sequence of Fig. 2 of Laux et al.

```

-----
1 MGSLEMVPMGAGPPSPGGDPDGYDGGNNSQYPSASGSSGNTPTPPNDEERESNEEPPPPY 60
      .               .               .               .
      20               40               60

-----
61 EDPYWGNGDRHSDYQPLGTQDQSLYLGLQHDGNDGLPPPPYSPRDDSSQHIYEEAGRGS 120
      .               .               .               .
      80              100              120

-----
121 NPVCLPVIVAPYLFWLAIAASCFTASVSTVVTATGLALSLLLLAAVASSYAAAQRKLLT 180
      .               .               .               .
      140             160             180

-----
181 PVTVLTAVVTTFFAICLTWRIEDPPFNSLLFALLAAAGGLQGIYVLVMLVLLILAYRRRWR 240
      .               .               .               .
      200             220             240

-----
241 RLTVC GGIMFLACVLVLIVDAVLQLSPLLGA VTVVSM TLLLLAFVLWLSSPGGLGTLGAA 300
      .               .               .               .
      260             280             300

1 -----MARRLPKPTLQGRLEADFPD SPLL PKFQELNQN NLPN 37
      M + TL L S L K L + L
301 LLTLAAALALLASLILGTLNLT T MFLMLLWTLV VLLICSSC S CPLSK=ILLARLFL=Y 358
      .               .               .               .
      320             340

      40      60      80
38 DVFREAQRSYLVLFTLSQFCYEEYVQRTFGVPRRQRAIDKRQRASVAGAGAHHLGGSSAT 97
      + S L+ S + + A + A GS
359 ALALLLLASALIAGGSILQTNFKSLSTEFIPNLF CMLLLIVAGILFILAILTEWGSGNR 418
      360      380      400
      100      120      140
98 PVQQAQAAASAGTGALASSAPSTAVAQSATPSVSSSISSLRAATSGATAAASAAA VDTG 157
      +A + T ++ + + + L A
419 TYGPVFMCLGGLLTMVAGAVWLT VMSNTLLSAWILTAGFLIFLIGFALFGVIRCCRYCCY 478
      420      440      460
      160
158 SGGGGQPHDTAPRGARKKQ* 177
      + + P R *
479 YCLTLESEERPPTPYRNTV* 498
      480

```

% Identity = 4.6 (23/500) % Homology = 3.2 (16/500) % Total = 7.8 (39/500)

///

9310-13DVCTDV SEQ ID NO 4.xprt x Laux et al. EBV terminal gene.xprt => Protein Alignment

Protein sequence 346 aa MLSGNAGEGATA ... FCEELLNKRVA\*

Protein sequence 498 aa MGSLEMVPMGAG ... ERPPTPYRNTV\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 4.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:3 (SEQ ID NO:4) with the amino acid sequence encoded by the nucleotide sequence of Fig. 2 of Laux et al.

```

      20      40
1 MLSGNAGE-GATACG-GSAAAGQDLISVPRNTFMTLLQTNLDNKPPRQTPLPYAAPLPPF 58
  M S      GA      G      G D + + +      N      P +      P PP+
1 MGSLEMVPMGAGPPSPGGDPDGYDGGNNSQYPSASGSSGNTPTPPNDEERESNEEPPPPY 60
      20      40      60
60      80      100
59 SHQAIATAP--S-YGP-GAGAVAPAGGYFTSPG-GYYAGPAGG-DPGAFLAMD-AHTYHP 111
      S Y P G + G      G      P      D + + A
61 EDPYWGNDRHSYQPLGTQDQSLYLGLQHDGNDGLPPPPYSPRDDSSQHIYEEAGRSM 120
      80      100      120
120      140      160
112 HPHPPPAYFG--LPGLFGPPPPCLLTDSHLRADYVPAPSRSNKRKRDPDEEGGGLF- 168
  +P P      L L      C + S +      A S      L
121 NPVCLPVIVAPYFLWLAIAASCFTASVSTVVTATGLALSLLLLAAVASSYAAAQRKLLT 180
      140      160      180
180      200      220
169 PGEDATLYRKDIAGLSKSVNELQHTLQALRRETLSYGHTGVGYCPQQGPCYTHSGPYGFQ 228
  P      T      A      E      L + G      Y      + ++
181 PVTVLTAVVTFFAICLTWRIEDPPFNSLLFALLAAAGGLQGIYVLVMLVLLILAYRRRW 240
      200      220      240
240      260      280
229 PHQSYEVPRIVPHPPPPPTSHQAAQAQPPPPGTQAPEAHCV-AESTIPEA-GAAGNSGPR 286
      ++      +      T      + A      + G G G
241 RLTVCGGIMFLACVLVLIVDAVLQLSPLLGAVTVVSMTLLLLAFVLWLSSPGGLGTLGAA 300
      260      280      300
300      320      340
287 EDTNPQQPTTEGHHRGKKLVQASASGVAQSKEPTTPKAKSV-SAHLKS-IFCEELLNKR 344
  T      L + +      S S+ S I L +
301 LLTIAAALALLASLILGTNLTTMFLMLLWTLVLLICSSSCSSCPLSKILLARLFLYAL 360
      320      340      360

345 A*----- 346
  A
361 ALLLLASALIAGGSILQTNFKSLSTEFIPNLFMCLLLIVAGILFILAILTEWGSNGRTY 420
      380      400      420

-----

421 GPVFMCLGGLLTMVAGAVWLTVMSTLLSAWILTAGFLIFLIGFALFGVIRCCRYCCYYC 480
      440      460      480

-----

481 LTLESEERPPTPYRNTV* 498

```

% Identity = 10.0 (50/498) % Homology = 4.8 (24/498) % Total = 14.9 (74/498)

///

9310-13DVCTDV SEQ ID NO 5.xprt x Laux et al. EBV terminal gene.xprt => Protein Alignment

Protein sequence 24 aa AVDTGSGGGGQP ... HDTAPRGARKKQ

Protein sequence 498 aa MGSLEMVPMGAG ... ERPPTPYRNTV\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 5.** Comparison of the amino acid sequence of SEQ ID NO:5 with the amino acid sequence encoded by the nucleotide sequence of Fig. 2 of Laux et al.

```

      20
1 AVDTGSGG-G-GQPHDTA-PRGARKKQ----- 24
      G G P      P G
1 MGSLEMVPMGAGPPSPGGDPDGYDGGNNSQYPSASGSSGNTPTPPNDEERESNEEPPPPY 60
      20              40              60
-----
61 EDPYWGNDRHSDYQPLGTQDQSLYLGLQHDGNDGLPPPPYSPRDDSSQHIYEEAGRGS 120
      80              100              120
-----
121 NPVCLPVIVAPYLFWLAAIAASCFTASVSTVVTATGLALSLLLLAAVASSYAAAQRKLLT 180
      140              160              180
-----
181 PVTVLTAVVTFFAICLTWRIEDPPFNSLLFALLAAAGGLQGIYVLVMLVLLILAYRRRWR 240
      200              220              240
-----
241 RLTVCGGIMFLACVLVLIVDAVLQLSPLLGA VTVVSM TLLLLAFVLWLSSPGGLGTLGAA 300
      260              280              300
-----
301 LLTLAAALALLASLILGTNLNLTMTFLLMLLWTLVLLICSSSCSSCPLSKILLARLFLYAL 360
      320              340              360
-----
361 ALLLLASALIAGGSILQTNFKSLSSSTEFIPNLFCMLLLIVAGILFILAILTEWGSNGRTY 420
      380              400              420
-----
421 GPVFMCLGGLLTMVAGAVWLTVMSNTLLSAWILTAGFLIFLIGFALFGVIRCCRYCCYYC 480
      440              460              480
-----
481 LTLESEERPPTPYRNTV* 498

```

% Identity = 1.0 (5/498)      % Homology = 0.0 (0/498)      % Total = 1.0 (5/498)

///

9310-13DVCTDV SEQ ID NO 6.xprt x Laux et al. EBV terminal gene.xprt => Protein Alignment

Protein sequence 30 aa STAVAQSATPSV ... LRAATSGATAAA

Protein sequence 498 aa MGSLEMVPMGAG ... ERPPTPYRNTV\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

Alignment 6. Comparison of the amino acid sequence of SEQ ID NO:6 with the amino acid sequence encoded by the nucleotide sequence of Fig. 2 of Laux et al.

```

-----
1 MGSLEMVPMGAGPPSPGGDPDGYDGGNNSQYPSASGSSGNTPTPPNDEERESNEEPPPPY 60
   .                20                .                40                .                60
-----
61 EDPYWGNDRHSDYQPLGTQDQSLYLGLQHDGNDGLPPPPYSPRDDSSQHIYEEAGRGS 120
   .                80                .                100               .                120
-----
121 NPVCLPVIVAPYLFWLAAIAASCFTASVSTVVTATGLALSLLLLAAVASSYAAAQRKLLT 180
   .                140               .                160                .                180
-----
181 PVTVLTAVVTFFAICLTWRIEDPPFNLSLLFALLAAAGGLQGIYVLVMLVLLILAYRRRWR 240
   .                200               .                220                .                240
-----
241 RLTVC GGIMFLACVLVLIVDAVLQLSPLLGA VTVVSM TLLLLAFVLWLSSPGGLGTLGAA 300
   .                260               .                280                .                300
-----
301 LLTLAAALALLASLILGTNLNLTTFLLMLLWTLVVLICSSCSCPLSKILLARLFLYAL 360
   .                320               .                340                .                360
-----
361 ALLLLASALIAGGSILQTNFKSLSTEFIPNLF CMLLLIVAGILFILAILTEWGSNRTY 420
   .                380               .                400                .                420
-----
1 -----STAVAQSATPSV 12
   +
421 GPVFMCLGGLLTMVAGAVWLTVMNLTLLSAWILTAGFLIFLIGFALFGVIRCCRYCCYYC 480
   .                440               .                460                .                480
   20
13 SSSISSLRAATSGATAAA 30
   + S R T
481 LTLESEERPPTPYRNTV* 498

```

% Identity = 0.6 (3/498)      % Homology = 0.4 (2/498)      % Total = 1.0 (5/498)

///

9310-13DVCTDV SEQ ID NO 1.xdna x Bankier et al. EcoRI Dhet fragment.xdna => DNA Parallel

DNA sequence 538 bp catgatggcacg ... aaacagtagccc linear

DNA sequence 12436 bp gaattctcaaag ... tgtttagaattc linear

Method: Blocks (Martinez)  
Layout: Standard  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Translation: Off

Alignment 7. Comparison of nucleotide sequence of SEQ ID NO:1 with the nucleotide sequence of Fig. 2 of Bankier et al.

```

-----
1  gaattctcaaaggcggcaccctcgccggcgcgccctgtcctcccagggacccgagacgaag 60
    .                20                .                40                .                60
-----
61  gcccgctctgtagaggaagtgggttgcgcattgcggggccagctcccagtagaccacgtccccc 120
    .                80                .                100               .                120
-----
121 cagacgcgcaggcacagggtctcggtcagggtctcgctctgttgccaggcaggactgc 180
    .                140               .                160               .                180
-----
181 agcttggccagaccctcggtggccacctggcgaggtactgctccttgcgcttgagcgcg 240
    .                200               .                220               .                240
-----
241 tccgagagggcgccggacggggccggggtctcgtgccccagccggccggggcacctccggg 300
    .                260               .                280               .                300
-----
301 ctctcccggaagcctcctcctcgccctcgccccaaccgctgcatggctcggttgagccgc 360
    .                320               .                340               .                360
-----
361 gtgtacagctcggttcctcttttgcaggatggcccggtactgggggtgcgccgtgaaggcg 420
    .                380               .                400               .                420
-----
421 gcggcgagtcgcgcttcagcgcctccaccgctcgcccgaggagctgtagaccccgccg 480
    .                440               .                460               .                480
-----
481 cagaagagccgctccgtggccccgggagccacggcggtcaaacaggtagtcagccttgcc 540
    .                500               .                520               .                540
1  -----catg 4
    |
541 cccgccagcgcctcctcgccaggccccccgcaccagggccaggcgacgctcccgggc 600
    .                560               .                580               .                600

```



```

      20
5  atggcagcgcggctgcccaag-c-ccaccctcc----- 35
   | | | | | | | | | | | | | | | | | | | |
601 agggcagagaggcggaatggccgccaccctccccctgccccgttgacccgatagcatgg 660
      620      640      660
-----
661 ccgccagagttccaatagaggagctccgagagctccgccacctccgggggcactgtcgag 720
      680      700      720
-----
721 aagacgttgtaggtgtccagcgctctggctgccccctctgcctccggccgccccggggccc 780
      740      760      780
-----
781 gggaccgcgcctctctctggggccgcccggcctcgcttctctctcagcctccaacaggtgc 840
      800      820      840
-----
841 ccgagccccgcctggcgggacttcattctcaaacagtcccgagaccggctccggattcacc 900
      860      880      900
-----
901 ggcaccgccaggtggttacaggagacgtgggtccccctctgccgtggaagggttgccgtgg 960
      920      940      960
-----
961 ttgggcagaaccatcagctcgcccacacagcgccagcagggcacagaggtgatgtagagg 1020
      980      1000      1020
-----
1021 cgcgggtctgggatgggacttacgccccgaaagcggcccagcagatccaggggcccggttc 1080
      1040      1060      1080
-----
1081 aggtctctccagccccatgggtgtgagacatgcaataaaacacgctattgattctcttcatt 1140
      1100      1120      1140
-----
1141 aaaatctctatgtcattttattaggcacaaacttacatcgactttatgccccccgtaaaac 1200
      1160      1180      1200
36 -----a 36
1201 tccacagagtacgcgactgagggggtacggagaggcgggacccgggtaccctttctacca 1260
      1220      1240      1260
      40
37 ggggag----- 42
   | | | | |
1261 ggggcgagcagcgcggcagaggcctctctcgagttctctagcaggtgcaccagctccagg 1320
      1280      1300      1320
-----
1321 gacagggcgctgcatgcacggtcattctgccgtctcaaacggggaaggaggatggcctcc 1380
      1340      1360      1380

```

1381 agctcgggccagcaggccggcggttgcgccaccgcagccacgtccagactccgggggtcc 1440  
 . 1400 . 1420 . 1440

1441 agccgggtgcacacgctcagctcaaccgccaggcgctacacctggctgtacgccgcgcgc 1500  
 . 1460 . 1480 . 1500 .

1501 agcagccccgacatcgccgccccaggggtctctagacctcgagtcgggggagaacggtgg 1560  
 . 1520 . 1540 . 1560

1561 ccagacggcgcttgcggtctgccccggagccctgcctcctccaccagcagcagccgg 1620  
 . 1580 . 1600 . 1620

1621 ccgaggcctgcgacgcgggtgctgaccggctcggccacgctgataaagtgtctctgggctg 1680  
 . 1640 . 1660 . 1680

1681 ccccgggcccccacactccctccagaaagtcccgagcggcctccgcggtccactcta 1740  
 . 1700 . 1720 . 1740

43 ---gctggaggc----- 51  
 |||||  
 1741 tcccgctggaggcgaatggtcgccagggtttctaggacgctgtccgccaggacggagaagc 1800  
 . 1760 . 1780 . 1800

1801 ggccaataagtactccgcgctgctccctagtcagcgaggcgcatgcctcgcccatggcat 1860  
 . 1820 . 1840 . 1860

1861 ccacaaggttgacaccacatcaaacacacagtgcttctcctgtttttgtgatataatgg 1920  
 . 1880 . 1900 . 1920

1921 cctccaggccagccctgatgtttctcaatctcatatgtggtcgcggcttggttcgggcgct 1980  
 . 1940 . 1960 . 1980

1981 tcacggtcaaccctaggggtgggggtggcaagacaaacttcttccgcatggaagagcccc 2040  
 . 2000 . 2020 . 2040

[illegible]

2101 ccataaaagtatcccaggttcccggcctggaatatctggttggtgcggttgacccccgtgt 2160  
 . 2120 . 2140 . 2160

```

52 -----ggattttc-cagac 64
2161 acttgttgatgggtcactggcagcgtgacaaccggacgggccttgacagacctggctaagac 2220
      2180      2200      2220
65 agtccccctgcttcctaaatttcaagagctgaaccagaataatctccccaatgatgttttt 124
      80      100      120
2221 agtc=====tgtggccgcgcag=accaccgt==ggt=cgcagt=aagggagg 2262
      2240      2260
125 cgggagggtcaaagaagttacctggtattttctgacatcccagttctgctacgaagagtac 184
      140      160      180
2263 aggtggcctccgcgtag==gcc==g==ctgccgac=tccaccgcccgc=gtgccagtag 2314
      2280      2300
185 gtgcagaggacttttggggtg-----cctcggc-----gccaacg 219
      200
2315 gtgggg=gtagtcacgggcgggcaccgactgcgtcctcggcaccagtcctgaatcaggc 2373
      2320      2340      2360
220 cgccatagacaagaggcagagagccagtggtggctggggctggtgctcatgcacaccttg 279
      240      260
2374 tgatgtagaactgggtctggccgcacgccttcaggatggcgttggtgagcctctgcttg 2433
      2380      2400      2420
280
280 cg-----ggtcacccgc 292
2434 cgtaagtgaccaggttgccaggcaccacatctatgacgttgctctcttcgtgggcccggg 2493
      2440      2460      2480
300
293 a-ccccgtcca----- 303
2494 agcccccgctccacaaagagggccagggtcagagtactcctccgcgtggccccgctgggga 2553
      2500      2520      2540
-----
2554 cagggaccgagcgcgcctggaaaagttgtgccacaggtacaggcttgagagcttagtgt 2613
      2560      2580      2600
-----
2614 ccgggaatagggtcttgtggttaggtgttgaggaatttcagttagggcccgttgatgatgt 2673
      2620      2640      2660
-----
2674 agttctccctcctggttagtgacttgatgaagctgttctggaggcggcattctcccccg 2733
      2680      2700      2720
-----
2734 tgaagaccacctgttcttgatcttgatgttcctggggcacagcatcagcaccttgga 2793
      2740      2760      2780
-----
2794 tgcgcacaggcagccgcccggccgtacaccggccctgcaggcgccgtccagggtctggca 2853
      2800      2820      2840
-----
2854 ggtcgcaggtgggctcccatgcaccaccttgccctccttgccgtgaggaccccccttgt 2913
      2860      2880      2900

```

```

304 -----gcaggctc----- 311
      |||||
2914 cgatggccaggctcctaagttggtgcacagcgtcttggtagtgaccctttagccactctg 2973
      2920                2940                2960
-----
2974 gggggctctggccaagcccggttgctcattctcatagcacatacagatgggcagggaga 3033
      2980                3000                3020
-----
3034 tgtcctgcaggatggtcagcagtgagcggtaaaacagctgggtgaagatggggcaggcgg 3093
      3040                3060                3080
-----
3094 gctgcgcaaaggggttgacagagtactgcatcacgtggtagcagctcttgaccaggctcct 3153
      3100                3120                3140
-----
312 -----aggccg 317
      |||
3154 tgtaggatgatgttgttcttgccatgctgttcataaaactggaccacttcggcgctccaccg 3213
      3160                3180                3200
      320
318 ccgcatcc----- 325
      |||||
3214 ccgcatccacgtccttgaacatcttgacaaaagtcacgcggggccatggggctccttctcta 3273
      3220                3240                3260
-----
3274 gctttccttcagcgtctatgccagccgagacagccgctccagcaggttctggttcagct 3333
      3280                3300                3320
-----
3334 gccagtaggtgtagcggggctcgtcgtccggccgctgcccgctcctccttatcgatga 3393
      3340                3360                3380
-----
3394 agttgagaaagttgcccaaaaagtccgtctcgttgtaggagcccgaggcccccagatca 3453
      3400                3420                3440
-----
326 -----gctgg----- 330
      ||||x
3454 catagggggtccctccgctgcgtggacatgacgggggggaagcgggtccctcagcctaaaga 3513
      3460                3480                3500
-----
3514 agagcgtgttcaggcacacggccggggcccgccctcgcagagcgagcacatgggactgg 3573
      3520                3540                3560
-----
3574 cggccgcccccgccacgtagctgcccgctctccggcaccggggtcagagagctcttctgtc 3633
      3580                3600                3620
-----
3634 cctggcaaaaactgcaggtagtaggcatacgggcaagaaggttgggcgagaaggaggccg 3693
      3640                3660                3680

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3694 catagaccaggtgctccacagcgtagtttcccggaccggtgggttccgggtcacgtctggcc 3753  
3700 3720 3740  
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3754 caccacagcccagagaagcagggtcggcgccaggggtcccagggtcccctcctgcaggggtcc 3813  
3760 3780 3800  
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3814 ccaggccggtgggtcatgtagaaactgttaaagagactctccttgccctgaccggttgact 3873  
3820 3840 3860  
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3874 tcgagacccccgagacgtagaggacggaattgggtggcaaagatctgcgtggacacgtggg 3933  
3880 3900 3920  
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3934 gggccaggctggcattatatcggtgtaacgcagccacacgggcctctggaccctcacagt 3993  
3940 3960 3980  
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3994 cggcaaacagggggccacgagtcgtagttgaggctggccgggggtctcgtgcgaggcctcca 4053  
4000 4020 4040  
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4054 gcattggcggtgcgtagctcaccgccagctcgcattgccgcgctgtccacaatcattaagg 4113  
4060 4080 4100  
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4114 ctcccagagtcgggtgactgatgggtgaggctgggaactccttgaggggggcccaccttgg 4173  
4120 4140 4160  
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4174 ccaccttggcctgggtcctgcaggctctgcttctccagcagctccaccagcttgcccaccc 4233  
4180 4200 4220  
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4234 gtccgacgcgcagcgctgcgccagcccgggtgtacagcgctcgtgcattgcagcggctga 4293  
4240 4260 4280  
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4294 ggtccgagttgtaaaactggcgagctggggcacgccctctgggaacacctccttgctgt 4353  
4300 4320 4340  
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4354 agagcgggaccctaacgctcgcagactgccccaccgctacctcctgttttaacgatggaa 4413  
4360 4380 4400  
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4414 tggccaccaggtttccgctgtagagtcgctccttgaaggcctcggttattgccaccgccc 4473  
4420 4440 4460  
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5194 ccactgtgtagcacagcaccaccctgagccgcgaccagtagtcgtagtggctcgttggtaca 5253  
5200 . 5220 . 5240 .

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 5254 ctgcgcgcaggacgctgatgatgagccgtacgtgcgtgtctttgcccccgatgtcggctg 5313  
       5260                              5280                              5300  
 -----

5314 tcctgcaggccagctccgcgtacagcttcctatccttcctcaggaggccttgatgagcc 5373  
       5320                              5340                              5360  
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5374 ggcagaggaccagggctggcaaaggcaggtctttctcatcccggtgaacaccgcgtaca 5433  
       5380                              5400                              5420  
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5434 tggccctgaacatgaggttagctggactcagccaccttgctcgtccggcgaggcgcgca 5493  
       5440                              5460                              5480  
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331 -----gaccgggg----- 338  
           |||||  
 5494 cccacgcctcgaccggggtcctcacaacacagaatctgtagacttggtggcctcatgg 5553  
       5500                              5520                              5540  
 -----

5554 tctcgtcaggccagctcacgggcttcaggcttatatgataaaatgggcgtggcagaatag 5613  
       5560                              5580                              5600  
 -----

5614 tataagacgcgaggcctgggtgaggagagtccagagcaatggccaggttcacgcctcagc 5673  
       5620                              5640                              5660  
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5674 tcctcctgttggcctcctgtgtggccgccggccaggctgtcacccgctttcttgggtgagc 5733  
       5680                              5700                              5720  
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5734 gagtcaccctgacctcctactggaggaggggtgagcctcgggtccagagattgaggtcagct 5793  
       5740                              5760                              5780  
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5794 gggtttaaactgggcccaggagaggagcaggtgcttattgggcgcacatgcaccacgatgtca 5853  
       5800                              5820                              5840  
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5854 tctttatagagtggcctttcaggggcttctttgatatccacagaagtgccaacaccttct 5913  
       5860                              5880                              5900  
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5914 ttttagtagtcaccgctgccaacatctcccatgacggcaactacctgtgccgcacatgaaac 5973  
       5920                              5940                              5960  
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5974 tgggcgagaccgaggtcaccaagcaggaacacctgagcgtggtgaagcctctaacgctgt 6033  
       5980                              6000                              6020  
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 6034 ctgtccactccgaaagggtctcagttcccagacttctctgtccttactgtgacatgcaccg 6093  
       6040                                  6060                                  6080

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 6094 tgaatgcatttccccatccccacgtccagtggtcatgcccagggcggtggagcccgac 6153  
       6100                                  6120                                  6140

-----  
 6154 caactgctggcaaatggcggtgttatgaaggaaaaggatgggagcctctctgttgctgttg 6213  
       6160                                  6180                                  6200

-----  
 6214 acctgtcacttcccaagccctggcacctgccagtgacctgcgttgggaaaaatgacaagg 6273  
       6220                                  6240                                  6260

-----  
 6274 aggaagcccacggggtttatgtttctggatacttgtcgcaataaacgcacttgcctat 6333  
       6280                                  6300                                  6320

-----  
 6334 caccttgtttttagtgtggcattgggggggtggcattgcgggtggatagcctcgcgactcg 6393  
       6340                                  6360                                  6380

-----  
 6394 tgggaaaaatggcggaaggggcacctggtgggaaaaatagttccaggtgacagcagcagtgtgt 6453  
       6400                                  6420                                  6440

-----  
 6454 gaagattgtcacagctgctggtttggagaaaaacgggggtgggcggtgatcaggggagaaca 6513  
       6460                                  6480                                  6500

-----  
 6514 attccccggggacacctgcacgagaccctgggctctcaggaactccgcccagggtcttgc 6573  
       6520                                  6540                                  6560

-----  
 6574 caattggggtgatcctgtagcgccgcggtttcagcatcacagggttattttgcctgaagct 6633  
       6580                                  6600                                  6620

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 6634 tgctggggcgtaaatccctctcgccttggtttctcagagagcatttcaggccggttttgca 6693  
       6640                                  6660                                  6680

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 6694 gtcgctgctgcagctatggggtccctagaaatggtgccaatgggcgcgggtccccctagc 6753  
       6700                                  6720                                  6740

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 6754 cccggcgggggatccggatgggtacgatggcggaacaactcccaatatccatctgcttct 6813  
       6760                                  6780                                  6800



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6814 ggctcttcttgggaacacccccacccacccaacgatgaggaacgtgaatcctaataagag 6873  
6820 . 6840 . 6860 .

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6874 cccccaccgccttatgaggacccatattggggcaatggcgaccgtcactcggactatcaa 6933  
6880 . 6900 . 6920 .

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6934 ccactaggaacccaagatcaaagtctgtacttgggattgcaacacgacgggaatgacggg 6993  
6940 . 6960 . 6980 .

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6994 ctccctccccctccctactctccacgggatgactcatctcaacacatatagaagaagcg 7053  
7000 . 7020 . 7040 .

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7054 ggcagaggaaggtaagagtgccatctatctgtactttttatttattgcatcacaaagtcaca 7113  
7060 . 7080 . 7100 .

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7114 tcaataataagggcgccatctagcgggagatgttatccacaccatcccaattcacatctc 7173  
7120 . 7140 . 7160 .

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7174 agggacaacaggtcaaagttctttgttgacacccccagcgctggctccaggggggtggaag 7233  
7180 . 7200 . 7220 .

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7234 cgttggatgcagtcctccgcacgccccggcgacgcctcctcccaacgcgtttctgaggatc 7293  
7240 . 7260 . 7280 .

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7294 agtcgctggctggtgggcatcggagtcggtggcggtcctccacggggacacgctccttc 7353  
7300 . 7320 . 7340 .

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7354 ttggccttgttctttgaccttttgacattcttctgaaggaacggcgagagtagcgtag 7413  
7360 . 7380 . 7400 .

-----  
7414 aatccagccagtggtctacccggtcgcacggttggtctttagatgaggagcaggcataaa 7473  
7420 . 7440 . 7460 .

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7474 agtccaaacaggacacagagtaccaccaggagtagtcttagtgctgacgtctgggtcc 7533  
7480 . 7500 . 7520 .

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7534 tcggggcaggggtggctaggcctggtctccgtagaagagccgggcaggccgcaggcagag 7593  
7540 . 7560 . 7580 .

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 7594 gactgctgctctagcaaagcacgctccaggacgtgtaccatctcgagagtgaggcacagc 7653  
           7600                                  7620                                  7640

-----  
 7654 tgttttcgtggactttttatacagtaaggacaaggaaagaaggccagaggaatgtggaaag 7713  
           7660                                  7680                                  7700

-----  
 7714 atgagcgaggacaggtgtggagggttttgggctagctcttagtttctgggtgtgagagagg 7773  
           7720                                  7740                                  7760

-----  
 7774 gattaaagtgtttatgcgcaaagaatgtgtcaacaacagggtgttcctgcctctgctggca 7833  
           7780                                  7800                                  7820

-----  
 7834 tgagttaggtgtggccttgggctgaatccaaatgtgtattggcacaagatggaaagcaaag 7893  
           7840                                  7860                                  7880

-----  
 7894 ttgctggagttactgggtgggagacagggatgtatgtgggtccccgcctggtatgccagta 7953  
           7900                                  7920                                  7940

                                  340  
 339 -----cct----- 341  
                                   |||  
 7954 ccctgtggaagtaaggggcctcatctgcctggtagttgtgttgtgcagaggtctgatgtg 8013  
           7960                                  7980                                  8000

-----  
 8014 tgtaggaggggtgggttcaacgcaggggcgttgggtggcggagtctggcaacgcccgggtc 8073  
           8020                                  8040                                  8060

-----  
 8074 cttgctacctgtgtgggtgtgttaagggctgggttaaagggtgtctgccaatctctgcatgtc 8133  
           8080                                  8100                                  8120

-----  
 8134 ctcccttcccttgttttgaaatagaatatgaatgtggcttttcagcctagacagacagt 8193  
           8140                                  8160                                  8180

-----  
 8194 gtggctaagggagtgtgtgccagtttaagggtgattagctaaggcattcccagtaaattggag 8253  
           8200                                  8220                                  8240

-----  
 8254 ggagagtcagtcaggcaagcctatgacatggtaatgcctagaagtaaagaaagggttagtc 8313  
           8260                                  8280                                  8300

                                                                                  360  
 342 -----tggcattcatcagcgcctcca-cggccg 368  
                                                           | | | | | | | | | | | | | | | |  
 8314 atagtagcttagctgaactgggcggtgggggtcgtcatcatc=====tccaccggaac 8366  
           8320                                  8340                                  8360

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      380              400              420
369 tagcccagtcgcgcgacccccctctgtttcttcatctattagcagcctccgggcccgcgactt 428
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
8367 cagaagaacccaaaagcagcgtaggaaggt=gtggatca=ccgccgccatggc=cggaat 8423
      8380              8400              8420
      440              460
429 cggggggcgactgccgcgcctccgcc-gccgcagccgtc----- 466
    |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
8424 c=atgactatgaccgccgcctccgtctgtcatcaaaggcgggccctggtcacctcctttg 8482
      8440              8460              8480
-----
8483 ttttcaacctcttccgtcaattgtggagggcctccatcatttccagcagagtcgctaggg 8542
      8500              8520              8540
-----
8543 ctatgaggcagcgggtcatgtgggccattgtcatcagtggtgtcagggtcctgtggggcca 8602
      8560              8580              8600
-----
8603 ttgtcatcagtggtgtcagggtcctgaggcagcgggtcatgtgggccattgtcatcagtg 8662
      8620              8640              8660
-----
8663 ttgtcagggtcctgtggggccattgtcatcagtggtgtcagggtcctgtggggccattgtca 8722
      8680              8700              8720
-----
8723 ggaccacctccaggtgcgcctaggttttgagagcagagtggggggtccgtcgccgggtcca 8782
      8740              8760              8780
-----
8783 ctcacgagcaggtggtgtctgcccctcgttgaggttagagtcagattcatggccagaatca 8842
      8800              8820              8840
-----
8843 tcggtagcttggttgaggggtgcgggagggagtcacgtggtggtgttcactgtgtcgt 8902
      8860              8880              8900
-----
8903 tgtccatggtaatacatccagattaaaatcgccagaaacaggaggagccaaaggagatca 8962
      8920              8940              8960
-----
8963 accaatagagtccaccagttttgtttagatagagagcaataatgagcaggatgaggtct 9022
      8980              9000              9020
-----
9023 aggaagaaggctaggaagaaggccaaaagctgccagatggtggcaccaagtgcgccagagc 9082
      9040              9060              9080
467 -----gatacc----- 472
      |||||
9083 atctccaataagtagatccagatacctaagactgcgttgaaaaaagagtgttaggggttg 9142
      9100              9120              9140

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9143 aaaagtgggggtgtggtaaataattcctaggggaatgttagatcttaccagtaagcacc 9202
      .               9160               .               9180               .               9200
-----

9203 gaagatgaacagcacacaattccaaggaacaatgcctgtccgtgcaaattccagagagcgat 9262
      .               9220               .               9240               .               9260
-----

9263 gagcaggaggggtgactgggggaaagaggagaaagtgcgttagagaaggaagagtaagggaa 9322
      .               9280               .               9300               .               9320
-----

9323 aggggggtgtggggcaaagggtgtaatacttactcatcagtaggagtatacaaagggtctcc 9382
      .               9340               .               9360               .               9380
-----

9383 aagtggacagagaagggtctcttctgaagataaagatgatcaaaattataattataagcat 9442
      .               9400               .               9420               .               9440
      480               .               500               .               520
473 -----gggt-caggtggcggggggacaaccccacgaca-ccgccccacgcggggga 520
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
9443 gagagcaaaggaatagaggacaaggaggggtcctccagtcacgtcactcataacgatgta 9502
      .               9460               .               9480               .               9500
-----

521 cgtaagaaaacagtagccc----- 538
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
9503 cagccaaaacagtagcgccaagaggaggagaaggagagcaaggcctaggggaagaggagag 9562
      .               9520               .               9540               .               9560
-----

9563 ggggggtcctcgagggggcgctcgcgggcccggtggggccctctcaaggtcgtgttccat 9622
      .               9580               .               9600               .               9620
-----

9623 cctcagggcagtggtgtcaggagcaaggcagttgaggaaagaagggggcagagcagtggtga 9682
      .               9640               .               9660               .               9680
-----

9683 gaggcttatgtagggcggttacgtcagagtaacgcgtgtttcttgggatgtaggcccggg 9742
      .               9700               .               9720               .               9740
-----

9743 gggatttgcggggtctgccggaggcagtagcggttacagatttcccgaagcggcggtgtg 9802
      .               9760               .               9780               .               9800
-----

9803 tgtgtgcatgtaagcgtagaaaaggggaagtagaaaagcgtgtgtttgtgttagaaaagcgg 9862
      .               9820               .               9840               .               9860
-----

9863 gtccccggggggcaagctgtgggaatgcggtggccaagtgaacaggaaatggaaaggca 9922
      .               9880               .               9900               .               9920

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10643 ggccccagggctgaccccggaacgtgacccggggctccggggtgacccagccaagcgt 10702  
 . 10660 . 10680 . 10700

10703	gaccaaggggcccgtgggtgacacagggaaccctgacaaaggccccccaggaaagacccc	10762
	10720 10740 10760	
-----		
10763	cggggggcatcgggggggtggggcatggggggccgcgcattcctggaaaaagtggaggggg	10822
	10780 10800 10820	
-----		
10823	cgtggccttcccccgcgccccccagccccccgcacagagcggcgctacggcgggcggg	10882
	10840 10860 10880	
-----		
10883	cggcgggggggtcgggggtccgcggggtccggggggtgcgggcgggtggatggcggcggacgt	10942
	10900 10920 10940	
-----		
10943	tccggggatcgggggggtcggggggcgccgcgcgggcgcagccatgcgtgaccgtgatga	11002
	10960 10980 11000	
-----		
11003	gggggcagggtcgcaggggggtgtgtctggtggggggcgggagcggggggcggcgcgggagc	11062
	11020 11040 11060	
-----		
11063	ctgcacgccgttgaggggtagaatgacagggggcggggacagagaggcggtcgcgccccc	11122
	11080 11100 11120	
-----		
11123	ggccgcgccagccaagcccccaaggggggcggggagcgggcaatggagcgtgacgaagg	11182
	11140 11160 11180	
-----		
11183	ccccagggtgaccccggaacacgtgacccggggctccgggggtgaccagccaagcgtga	11242
	11200 11220 11240	
-----		
11243	ccaaggggcccgtgggtgacacagggaaccctgacaaaggccccccaggaaagacccccg	11302
	11260 11280 11300	
-----		
11303	tggggcatggggggccgcgcattcctggaaaaagtggagggggcgtggccttcccccg	11362
	11320 11340 11360	
-----		
11363	gccccccagccccccgcacagagcggcgctacggcgggcgggcggcgggggtcgggggt	11422
	11380 11400 11420	
-----		
11423	ccgcggggtccggggggtgcgggcgggtggatggcggcggacgttccggggatcggggggg	11482
	11440 11460 11480	

11483 tcgggggggcgcccgcgcggcgccagccatgcgtgaccgtgatgagggggcagggtcgcagg 11542  
                  .                11500                       .                11520                       .                11540

11543 ggggtgtgtctggtgggggcgggagcggggggcggcgcgggagcctgcacgccgttgagg 11602  
          .                11560               .                11580               .                11600

11603 gtagaatgacagggggcggggacagagaggcggtcgcgcccccggcgcgccagccaagc 11662  
 . 11620 . 11640 . 11660

11663 ccccaagggggcggggagcgggcaatggagcgtgacgaagggccccagggtgaccccg 11722  
 . 11680 . 11700 . 11720

11723 gcaaacgtgaccgggggctccggggtgaccagccaagcgtgaccaaggggcccggtgggt 11782  
 . 11740 . 11760 . 11780

11783 gacacaggcaaccctgacaaaggccccccaggaaagacccccggggggcatcggggggtg 11842  
 . 11800 . 11820 . 11840

11843 gggcatggggggcgcgcattcctggaaaaagtggagggggcgtggccttccccgcggc 11902  
 . 11860 . 11880 . 11900

11903 cccccagccccccgcacagagcgggcgctacggcgggcgggcgggcggggtcgggggtcc 11962  
 . 11920 . 11940 . 11960

11963 gcgggctccgggggctgcgggcggtggatggcggcggacgttccggggatcgggggggtc 12022  
 . 11980 . 12000 . 12020

12023 ggggggagcgccgcgcggggcgcagccatgcgtgaccgtgatgagggggcagggtcgcagggg 12082  
          ·                12040               ·                12060               ·                12080

12083 gtgtgtctcgggtgggggaggagcggggggcggcgcgggagcctgcacgccgttgagggt 12142  
 . 12100 . 12120 . 12140

12143 agaatgacagggggcggggacagagaggcggtcgcgccccggccgcgccagccaagccc 12202  
                  12160                  12180                  12200

12203 ccaaggggggaggggagcgggcaatggagcgtagacgaagggcccagggtgacccggc 12262  
          .               12220                .               12240                .               12260

12263 aaacgtgacccggggctccggggtgaccagccaagcgtgaccaaggggcccggtgggtga 12322  
 . 12280 . 12300 . 12320

12323 cacaggcaaccctgacaaaggccccccaggaaagacccccggggggcatcgggggggtg 12382  
 . 12340 . 12360 . 12380

12383 ttggcgggggcatgggggggtcggatttcgcccttattgccctgtttagaattc 12436  
          •                12400               •                12420               •

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% Identity = 2.3 (291/12474)
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///



9310-13DVCTDV SEQ ID NO 1.xdna x Bankier et al. EcoRI Dhet fragment complement.xdna => DNA Parallel

DNA sequence 538 bp catgatggcacg ... aaacagtagccc linear

DNA sequence 12436 bp gaattctaaaca ... ctttgagaattc linear

Method: Blocks (Martinez)  
Layout: Standard  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Translation: Off

**Alignment 8.** Comparison of nucleotide sequence of SEQ ID NO:1 with the complement of the nucleotide sequence of Fig. 2 of Bankier et al.

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-----
1  gaattctaaacagggcaataagggcgaaatccgaccccccatgccccgccaacacccc 60
    .                20                .                40                .                60
-----
61  ccccgatgcccccggggtctttcctggggggcctttgtcagggttgcctgtgtcaccc 120
    .                80                .                100               .                120
-----
121 acgggcccccttggtcacgcttggtcgggtcacccccggagccccgggtcacgtttgccggg 180
    .                140               .                160               .                180
-----
181 gtcagccctggggcccttcgtcacgctccattgcccgctccccgcccccccttgggggctt 240
    .                200               .                220               .                240
-----
241 ggctggcgcgggccggggggcgcgaccgcctctctgtccccgccccctgtcattctaccctc 300
    .                260               .                280               .                300
-----
301 caacggcgtgcaggctcccgcgccgccccccgctcccgccccaccagacacacccccctg 360
    .                320               .                340               .                360
-----
361 cgaccctgccccctcatcacggtcacgcatggctgcgccccgcgcgccgcccccgacccc 420
    .                380               .                400               .                420
-----
421 cccgatccccggaacgtccgcccgcacccacccgcccgcagcccccgagcccgcggaccc 480
    .                440               .                460               .                480
-----
481 cgaccccccgccgccccgccccgcccgtagcgccgctctgtcgggggggctggggggcccgcg 540
    .                500               .                520               .                540
-----
541 ggggaaggccacgccccctccactttttccaggaatgcgcgggccccccatgccccacccc 600
    .                560               .                580               .                600

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661 gggcccccttggtcacgcttggtgggtcaccccgagccccgggtcacgtttgccgggggt 720
    .                680                700                720
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721 cagccctggggcccttcgtcacgctccattgcccgtccccgcccccttgggggcttgg 780
    .                740                760                780
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781 ctggcgcgggccggggggcgcgaccgcctctctgtccccgccccctgtcattctaccctcca 840
    .                800                820                840
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841 acggcgtgcaggctccccgcgcgccccccgctcccgccccaccagacacacccccctgcg 900
    .                860                880                900
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901 accctgccccctcatcacgggtcacgcatggctgcgcccgcgcggcgccccccgaccccc 960
    .                920                940                960
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961 cgatccccggaacgtccgcgcgcatccaccgcccgcagcccccgagcccgcggacccccg 1020
    .                980                1000                1020
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1021 accccccgcgcgcgcgcgcgcgtagcgccgctctgtgcgggggggctggggggccgcggg 1080
    .                1040                1060                1080
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1081 ggaaggccacgccccctccactttttccaggaatgcgcggccccccatgccccacggggg 1140
    .                1100                1120                1140
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1141 tctttcctggggggcctttgtcaggggttgccctgtgtcacccacgggcccccttggtcacgc 1200
    .                1160                1180                1200
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1201 ttggctgggtcaccccgagccccgggtcacgtttgccgggggtcagccctggggcccttc 1260
    .                1220                1240                1260
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1261 gtcacgctccattgcccgtccccgcccccccttgggggcttggctggcgcgggccgggggc 1320
    .                1280                1300                1320
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1321 gcgaccgcctctctgtccccgccccctgtcattctaccctccaacggcgtgcaggctccc 1380
    .                1340                1360                1380
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### ► DNA Parallel

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                    1400                    1420                    1440

1441 cggtcacgcacatggctgcgcccgcgcggcgccccccgaccccccgatccccggaacgtcc 1500  
 . 1460 . 1480 . 1500

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 . 1520 . 1540 . 1560

1561 cgccgtagcgccgctctgtgcgggggggctggggggccgcgggggaaggccacgccccct 1620  
 . 1580 . 1600 . 1620

1621 ccactttttccaggaatgcgcggccccccatgccccacccccgatgccccccgggggtc 1680  
 . 1640 . 1660 . 1680

1681 tttcctgggggggcctttgtcaggggttgctgtgcacccacgggccccttggtcacgctt 1740  
 . 1700 . 1720 . 1740

1741 ggctgggtcacc<sup>ccg</sup>gagccccgggtcacg<sup>t</sup>ttgc<sup>c</sup>gggggtcagccctggggcccttcgt 1800  
                .<sup>.</sup>                1760                .<sup>.</sup>                1780                .<sup>.</sup>                1800

1801 c a c g c t c c a t t g c c c g c t c c c c g c c c c c c t t g g g g g c t t g g c t g g c g c g g c c g g g g g c g c 1860  
 . 1820 . 1840 . 1860

1861 gaccgcctctctgtccccgccccctgtcattctaccctccaacggcgtgcaggctccgc 1920  
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1921 gccgccccccgctcccgccccaccagacacaccccctgcgaccctgccccctcatcacg 1980  
 . 1940 . 1960 . 1980

1981 gtcacgcatggctgcgccccgcgcggcgcccccccgaccccccgatccccggaacgtccgc 2040  
 . 2000 . 2020 . 2040

2041 cgccatccaccgccccgcagcccccgaggcccgcggaccccgacccccgccgcccgcgccg 2100  
                        .                    .                    .                    .  
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2101 ccgtagcgcgcgctctgtgcgggggggctggggggccgcgggggaaggccacgccccctcc 2160  
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2221 tgcctcatgacactcgcacagccacacccttttgcctgaatcgcgcacctcattctga 2280  
 . 2240 . 2260 . 2280

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 . 2360 . 2380 . 2400

2401 cggcctcccgccctgccgccaacgacctcccaacgttgcgcgccccgcgcctctttgtgca 2460  
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 . 2480 . 2500 . 2520

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 . 2540 . 2560 . 2580

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 . 2600 . 2620 . 2640

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 . 2660 . 2680 . 2700

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2761 tgctctgcccccttcttttctcaactgccttgctcctgacacactgccctgaggatggaa 2820  
 . 2780 . 2800 . 2820

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2881 tcttccttaggccttgctctccttctcctctcttggcgctactgttttggctgtacatc 2940  
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 . 3440 . 3460 . 3480

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3841 acaggaccctgacaacactgatgacaatggcccacatgaccgctgcctcatagccctag 3900  
 . 3860 . 3880 . 3900

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 . 3980 . 4000 . 4020

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 . 4040 . 4060 . 4080

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4201 gccttagctaatcaccttaactggcacacactcccttagccacactgtctgttaggctg 4260  
 . 4220 . 4240 . 4260

4261 aaaagccacattcatatttctattttcaaaaacaaggggaaaggaggacatgcgagaattggc 4320  
 . 4280 . 4300 . 4320

4321 agacacctttaccagcccttaacacaccacacaggtagcaaggaccgcggcggttgccag 4380  
 . 4340 . 4360 . 4380

4381 actccgccaccaacgccccctgcgttgaaacccaccccctcctacacacatcagacctctgca 4440  
 . 4400 . 4420 . 4440

4441 caacacaactaccaggcagatgaggcccttactttccacaggggtactggcataccagcgg 4500  
                    .                4460                    .                4480                    .                4500

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4561 tgccaatacacatttggttcagcccaagccacacctaactcatgccagcagaggcagga 4620
      .               4580               .               4600               .               4620
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4621 acacctgttggtgacacattctttgcgcataagcactttaatccctctctcacaccaga 4680
      .               4640               .               4660               .               4680
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4681 aactaagagctagcccaaacctccacacctgtcctcgcctcatctttccacattcctctg 4740
      .               4700               .               4720               .               4740
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4741 gccttctttccttgctccttactgtataaaagtccacgaaaacagctgtgcctcactctcg 4800
      .               4760               .               4780               .               4800
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      .               4880               .               4900               .               4920
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 . 5420 . 5440 . 5460

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 . 5480 . 5500 . 5520

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 . 5540 . 5560 . 5580

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 . 5600 . 5620 . 5640

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 . 5780 . 5800 . 5820

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 . 5900 . 5920 . 5940

28 ---cacc----- 32

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6001 cctggaactatatttcccacggtgcccttcgcccattttcccacgagtcgcgaggctatc 6060  
 . 6020 . 6040 . 6060



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 6061 caccgcgaatgccaccccccaatgccacactaaaacaagggtgaaataggcaagtgcgtt 6120  
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6121 tattgcgacaagtatccagaaacataaacccccgtgggcttctctcttgcatttttccca 6180  
                                 6140                                6160                                6180  
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6181 acgcaggtcactggcagggtgccagggcttgggaagtgcagggtcaacagcaacagagagg 6240  
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6241 ctcccatccttttcttcataacaccgccatttgcgcagttggtgcgggctccacgccc 6300  
                                 6260                                6280                                6300  
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                                 6320                                6340                                6360  
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6361 aggacagagaagtctggaactgagaccttctggagtgagacagacagcgtagaggcttc 6420  
                                 6380                                6400                                6420  
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6421 accacgctcagggtgttctctgcttggtagacctcggtctcgcccagtttcatgcggcacagg 6480  
                                 6440                                6460                                6480  
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6481 tagttgccgtcatgggagatggtggcagcggtgactactaaaaagaagggtgttggcactt 6540  
                                 6500                                6520                                6540  
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6541 ctgtggatatcaaagaagccccctgaaaggccactctataaagatgacatcggtgcatg 6600  
                                 6560                                6580                                6600  
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6601 cgcccaataagcacctgctctctctctgggcccagtttaaacagctgacctcaatctct 6660  
                                 6620                                6640                                6660  
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33 -----tccag----- 37  
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                                 6680                                6700                                6720  
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                                 6740                                6760                                6780  
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6781 gccattgctctggactctctctcaccagggcctcgcttattatactattctgccacgcccc 6840  
                                 6800                                6820                                6840

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[illegible]

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[illegible]

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      8420      8440      8460
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8461 gcccggtgtggctgcgttacaccgatataatgccagcctggccccccacgtgtccacgcag 8520
      8480      8500      8520
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8521 atctttgccaccaattccgtcctctacgtctcgggggtctcgaagtcaaccggtcagggc 8580
      8540      8560      8580
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      64 -----cagt----- 67
      |||||
8581 aaggagagtctctttaacagtttctacatgaccacggcctggggaccctgcaggagggg 8640
      8600      8620      8640
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      68 -----ccctgcttc----- 77
      |||||
8641 acctgggaccctgcccggaccctgcttctcgggctggggggccagacgtgaccgga 8700
      8660      8680      8700
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8701 accaacgggtccgggaaactacgctgtggagcacctgggtctatgcggcctccttctcggcc 8760
      8720      8740      8760
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      8780      8800      8820
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8881 ctctgcgagggccggggcccggtgtgcctgaacacgctcttcttttaggctgagggac 8940
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      8960      8980      9000
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      9020      9040      9060
      80      100
78 -----cta-aatttcaag-agctgaaccagaa----- 102
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9061 gacgggcagcggccggacgacgagccccgctacacctaactggcagctgaaccagaacctg 9120
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 . 9260 . 9280 . 9300

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 . 9320 . 9340 . 9360

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 . 9380 . 9400 . 9420

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                9440                    9460                    9480

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 . 9560 . 9580 . 9600

9601 gccctgcagggccgggtgtacggccggcggtgcctgtgcgcattgtccaaggtgctgatg 9660  
 . 9620 . 9640 . 9660

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 . 9680 . 9700 . 9720

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 . 9800 . 9820 . 9840

9841 ctgtacctgtggcacaaacttttccaggcgggcgctcgggtccctgtccccagcggggccagc 9900  
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 . 9920 . 9940 . 9960

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140          160          180
138 gaagtta-cctg--gtatttctgacat-cccagttctgc-t-a-c--gaag-agt-ac-g 185
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      .          10040          10060          10080
      200
186 -tgcagaggacttttgggt----- 204
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
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      .          10220          10240          10260
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      .          10280          10300          10320
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10321 ctgggatactttatggcgccggcggtggacaggaacctgctgcaggcccccggggctggg 10380
      .          10340          10360          10380
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      .          10400          10420          10440
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      .          10460          10480          10500
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      .          10520          10540          10560
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10561 gtgtgcaaccttgatggatgccatggcgaggcatgcgcctcgctgactagggacgacgcg 10620
      .          10580          10600          10620
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10621 gagtacttattggccgcttctccgtcctggcgacagcgtcctagaaaccctggcgacc 10680
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      |||||
10801 gcgtcgcaggcctcggccgggctgctgctgggtggaggagggcagggctccgggggcaga 10860
      .           10820           .           10840           .           10860
      .
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10861 cgcaagcgccgtctggccaccgttctccccggactcgaggtctagagaccctggggcg 10920
      .           10880           .           10900           .           10920
      .
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10921 cgatgtcggggctgctggcgggcggtacagccaggtgtacgccctggcggttgagctga 10980
      .           10940           .           10960           .           10980
      .
-----
10981 gcgtgtgcacccggctggacccccggagtctggacgtggctgcgggtggtgcgcaacgccg 11040
      .           11000           .           11020           .           11040
      .
-----
11041 gcctgctggccgagctggaggccatcctccttccccgtttgagacggcagaatgaccgtg 11100
      .           11060           .           11080           .           11100
      .
-----
11101 catgcagcgccctgtccctggagctggtgcacctgctagagaactcgagagaggcctctg 11160
      .           11120           .           11140           .           11160
      .
-----
11161 ccgcgctgctcgcccctggtagaaagggtacccgggtcccgccctctccgtacccctcag 11220
      .           11180           .           11200           .           11220
      .
-----
11221 tcgcgctactctgtggagttttacggggggcataaagtcgatgtaagtttgtgcctaataa 11280
      .           11240           .           11260           .           11280
      .
-----
11281 atgacatagagattttaatgaagagaatcaatagcgtgttttattgcatgtctcacacca 11340
      .           11300           .           11320           .           11340
      .
-----
11341 tggggctggagagcctggaacgggcccctggatctgctgggcccgtttcggggcgtaagtc 11400
      .           11360           .           11380           .           11400
      .
-----
11401 ccatcccagaccgcgcctctacatcacctctgtgccctgctggcgctgtgtgggcgagc 11460
      .           11420           .           11440           .           11460
      .
-----
11461 tgatggttctgcccaccacggcaacccttccacggcagaggggaccacgtctcctgta 11520
      .           11480           .           11500           .           11520
```

-----  
 11521 accacctggcgggtgccgggtgaatccggagccgggtctcgggactgtttgagaatgaagtcc 11580  
                                   11540                                  11560                                  11580  
 -----

11581 gccaggcgggggctcggggcacctgttgaggctgaggagaaggcgaggccggggcgccag 11640  
                                   11600                                  11620                                  11640  
                                   220                                  240

213 -----gccaacgcgc-catagacaagaggcagagagccagtgtggctggggct 259  
                                   ||                                  ||                                  |||||

11641 aggagggcgcggtcccggggccggggcgggccggaggcagag===== 11681  
                                   11660                                  11680

260                                  280                                  300  
 260 ggtgctcatgcacaccttggcgggtcatccgccaccccgctccagcaggctcaggccgcc 319  
 =====

320                                  340                                  360  
 320 gcatccgctgggaccggggccttggcacatcagcgccgctccacggccgtagcccagtcc 379  
 =====

380                                  400                                  420  
 380 gcgacccccctctgtttcttcatctattagcagcctccgggcccgcgacttcggggggcgac- 438  
                                                                                   |||||

11682 =====ggggcgacc 11690  
 -----

11691 agagcgctggacacctacaacgtcttctcgacagtcccccgagggtggcggagctctcg 11750  
                                   11700                                  11720                                  11740

11751 gagctcctctattggaactctggcgccatgctatcggtgcaacggggcagggggagggt 11810  
                                   11760                                  11780                                  11800

11811 ggcggccattcccgcctctctgcccgtgttgcccgggagcgctgcctggccctggtgcgg 11870  
                                   11820                                  11840                                  11860

11871 ggggcctgcgaggaggcgctggcgggggcaaggctgactcacctgtttgacgccgtggct 11930  
                                   11880                                  11900                                  11920

11931 cccggggccacggagcggtcttctgcggcggggtctacagctcctcggggcgacgcggtg 11990  
                                   11940                                  11960                                  11980

439 -----tgccgcgcctccgcgcgcagccgtcgataaccggg--- 475  
                                   |||||

11991 gaggcgctgaaggcggactgcgcgcgccttcacggc=gcaccccag=taccgggcca 12048  
                                   12000                                  12020                                  12040

12049 tcctgaaaaagaggaacgagctgtacacgcgggtcaaccgagccatgcagcggttggggc 12108  
                                   12060                                  12080                                  12100



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-----
12109 gaggcgaggaggagggcgctcccgggagagcccggaggtgccccggccggctggggcacgag 12168
      .      12120      .      12140      .      12160

476 -----tc 477
      |
12169 agccccggcccgctccggcgccctctcggacgcgctcaagcgcaaggagcagtacctgcgcc 12228
      .      12180      .      12200      .      12220
480
478 aggtggc----- 484
      |||||
12229 aggtggccaccgaggggtctggccaagctgcagtcctgcctggcgcaacagagcgagaccc 12288
      .      12240      .      12260      .      12280
      .
485 -----gggggacaacccc-ac-gacacc-g-ccc-ca 511
      .      .      .      .      .      .      .      .      .      .
12289 tgaccgagaccctgtgcctgcgcgtctgggggacgtggtctactgggagctggcccgca 12348
      .      12300      .      12320      .      12340
      .
512 cgcggggc-acgtaagaaacagtagccc----- 538
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
12349 tgcgcaaccacttcctctacagacgggccttcgtctcgggtccctgggaggacaggcgcg 12408
      .      12360      .      12380      .      12400

-----

12409 ccggcgagggtgccgcctttgagaattc 12436
      .      12420

```

% Identity = 1.9 (243/12628)

///

9310-13DVCTDV SEQ ID NO 3.xdna x Bankier et al. EcoRI Dhet fragment.xdna => DNA Parallel

DNA sequence 1038 bp atgctatcaggt ... cgcgtggcttga linear

DNA sequence 12436 bp gaattctcaaag ... tgtttagaattc linear

Method: Blocks (Martinez)  
Layout: Standard  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Translation: Off

Alignment 9. Comparison of nucleotide sequence  
of SEQ ID NO:3 with the nucleotide sequence of  
Fig. 2 of Bankier et al.

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-----
1  gaattctcaaaggcggcaccctcgccggcgcgccctgtcctcccagggaacccgagacgaag 60
   .                20                .                40                .                60
-----
61  gcccgtctgtagaggaagtgggttgcgcattgcggggccagctcccagtagaccacgtccccc 120
   .                80                .                100               .                120
-----
121 cagacgcgcaggcacagggtctcggtcagggtctcgtctctgttgcgccaggcaggactgc 180
   .                140               .                160               .                180
-----
181 agcttgggccagaccctcgggtggccacctggcgccaggtactgctccttgcgcttgagcgcg 240
   .                200               .                220               .                240
-----
241 tccgagagggcgccgggacggggccgggctctcgtgccccagccggccggggcacctccggg 300
   .                260               .                280               .                300
-----
301 ctctcccgggagcgcctcctcctcgcctcggcccaaccgctgcatggctcggttgagccgc 360
   .                320               .                340               .                360
-----
361 gtgtacagctcgttccctcttttgcaggatggcccggtactgggggtgcgccgtgaaggcg 420
   .                380               .                400               .                420
-----
421 gcggcgagctccgccttcagcgccctccaccgcgctcgcccaggagctgtagaccccgcgg 480
   .                440               .                460               .                480
-----
481 cagaagagccgctccgctggcccccgggagccacggcgctcaaacagggtgagtcagccttgcc 540
   .                500               .                520               .                540
-----
541 cccgccagcgcctcctcgcaggcccccccgaccaggggccaggcgacgctcccgggcaaac 600
   .                560               .                580               .                600
```

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601 agggcagagagggcggaatggccgccaccctccccctgccccgttgccacgatagcatgg 660
    .               620               .               640               .               660
-----

661 ccgccagagttccaatagaggagctccgagagctccgccacctccgggggcactgtcgag 720
    .               680               .               700               .               720
-----

721 aagacgttgtaggtgtccagcgctctgggtcgccccctctgcctccggccgccccggggccc 780
    .               740               .               760               .               780
-----

781 gggaccgcgccctcctctggggcgcccgccctcgcccttctcctcagcctccaacaggtgc 840
    .               800               .               820               .               840
-----

841 ccgagccccgcctggcggaacttcatttctcaaacagtccccgagaccggctccggattcacc 900
    .               860               .               880               .               900
-----

901 ggcaccgccaggtggttacaggagacgtgggtccccctctgcccgtggaaggggttgccgtgg 960
    .               920               .               940               .               960
-----

961 ttgggcagaaccatcagctcgcccacacagcgccagggcacagaggtgatgtagagg 1020
    .               980               .               1000               .               1020
-----

1021 cgcgggtctggggatgggacttacgccccgaaagcgggccagcagatccagggcccgttcc 1080
    .               1040               .               1060               .               1080
-----

1081 aggctctccagccccatgggtgtgagacatgcaataaaacacgctattgattctcttcatt 1140
    .               1100               .               1120               .               1140
-----

1141 aaaatctctatgtcattttattaggcacaaaacttacatcgactttatgcccccgtaaaac 1200
    .               1160               .               1180               .               1200
-----

1201 tccacagagtacgcgactgaggggggtacggagaggcgggaccgggtaccctttctacca 1260
    .               1220               .               1240               .               1260
-----

1261 ggggcgagcagcgcggcagaggcctctctcgagttctctagcaggtgcaccagctccagg 1320
    .               1280               .               1300               .               1320
-----

1321 gacagggcgctgcatgcacgggtcatttctgccgtctcctcaaacgggggaaggaggatggcctcc 1380
    .               1340               .               1360               .               1380

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2101 ccataaagtatcccaggttcccggcctggaatatctggttggtgcggttgacccccgtgt 2160  
 . 2120 . 2140 . 2160

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1 -----atgctatcag----- 10

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2881 ccttggcctccttggccgtgaggaccccttgtcgatggccaggctcctaaagtgggtgc 2940  
 . 2900 . 2920 . 2940

3661 agcgggcaagaaggttgggcgagaaggaggccgcatagaccaggtgctccacagcgtagt 3720  
 . 3680 . 3700 . 3720

-----  
 3721 ttcccggaaccgttggttccgggtcacgtctggcccaccccagcccagagaagcaggggtcggc 3780  
                                   3740                                  3760                                  3780  
 -----

3781 ggcaggggtcccaggtcccctcctgcaggggtccccaggccgtgggtcatgtagaaactgt 3840  
                                   3800                                  3820                                  3840  
 -----

3841 taaagagactctccttgccctgaccgggttgacttcgagacccccgagacgtagaggacgg 3900  
                                   3860                                  3880                                  3900  
 -----

11 -----gta 13  
 3901 aattggtggcaaagatctgcgtggacacgtggggggccaggctggcattatatcgggtgta 3960  
                                   3920                                  3940                                  3960  
                                   |||||

14 acgc----- 17  
 3961 acgcagccacacggggcctctggaccctcacagtcggcacaacagggggccacgagtcgtagt 4020  
                                   3980                                  4000                                  4020  
 -----

4021 tgaggctggccggggtctcgtgcgaggcctccagcatggcgggtgcgtagctcaccgcca 4080  
                                   4040                                  4060                                  4080  
 -----

4081 gctcgcattgcgcgctgtccacaatcattaaggctcccagagtcggggtgactgatgggtg 4140  
                                   4100                                  4120                                  4140  
 -----

4141 aggctgggaactccttgagggggggccaccttgggccaccttggcctggtcctgcaggctct 4200  
                                   4160                                  4180                                  4200  
 -----

4201 gcttctccagcagctccaccagcttgcccacccgtcggacgcgcagcgcctgcgccagcc 4260  
                                   4220                                  4240                                  4260  
 -----

4261 cgggtgtacagcgcctcgtgcattgcagcggctgaggtccgagttgtaaaactggcggagct 4320  
                                   4280                                  4300                                  4320  
 -----

4321 ggggcacgcccctctgggaacacctccttgctcgtagagcgggaccctaacgctcgcagact 4380  
                                   4340                                  4360                                  4380  
 -----

4381 gccccaccgctacctcctgttttaacgatggaatggccaccagggtttccgctgtagagtc 4440  
                                   4400                                  4420                                  4440  
 -----

4441 gctccttgaaggcctcgggttattgccaccgccccccaggtaggcagagggatctagccctt 4500  
                                   4460                                  4480                                  4500  
 -----

5221 gccgcgaccagtagtcgtagtggtcgttgtagactgcgcgcaggacgctgatgatgagcc 5280  
 . 5240 . 5260 . 5280



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6001 aacacctgagcgtggtgaagcctctaacgctgtctgtccactccgaaagggtctcagttcc 6060  
 . 6020 . 6040 . 6060

6061 cagacttctctgtccttactgtgacatgcacggtgaatgcatttccccatccccacgtcc 6120  
 . 6080 . 6100 . 6120

6121 agtggctcatgcccgagggcgtagagcccgacccaactgcggcaaatggcggtgttatga 6180  
 . 6140 . 6160 . 6180

6181 aggaaaaggatgggagcctctctgttgctgttgacctgtcacttcccaagccctggcacc 6240  
 . 6200 . 6220 . 6240

6241 tgccagtgacctgcgttgggaaaaatgacaaggaggaagccacgggggtttatgtttctg 6300  
 . 6260 . 6280 . 6300

6301 gataacttgctgcgaataaacgcacttgcctatttcaccttgtttagtgtggcattggggg 6360  
 . 6320 . 6340 . 6360

6361 ggtggcattgcgggtggatagcctcgcgactcgtgggaaaatgggcggaagggcaccgtg 6420  
 . 6380 . 6400 . 6420

6421 ggaaaatagttccagggtgacagcagcagtggtgtgaagattgtcacagctgctggtttgga 6480  
 . 6440 . 6460 . 6480

6481 gaaaacgggggtgggcggtgatcaggggagaacaattccccggggacacctgcacgagacc 6540  
 . 6500 . 6520 . 6540

6541 cctgggctctcaggaactccgccaggtcttgccaattgggggtgatcctgtagcgccgcg 6600  
 . 6560 . 6580 . 6600

6601 gtttcagcatcacagggttattttgcctgaagcttgctggggcgtaaataccctctcgccctt 6660  
 . 6620 . 6640 . 6660

6661 gtttctcagagagcatttcaggccggttttgacgtcgctgctgcagctatgggggtcccta 6720  
 . 6680 . 6700 . 6720

6721 gaaatggtgccaatgggcgcgggtccccctagccccggcggggatccggatgggtacgat 6780  
 . 6740 . 6760 . 6780

6781 ggcggaacaactcccaatatccatctgcttctggctcttctgggaacacccccacccca 6840  
 . 6800 . 6820 . 6840

7561 tccgtagaagagccgggcaggccgacggcagaggactgctgctctagcaaagcacgctcc 7620  
                  .  
                       7580                  .  
                                       7600                  .  
                                               7620

7621 aggacgtgtaccatctcgagagtgaggcacagctgttttcgtggacttttatacagtaag 7680  
 . 7640 . 7660 . 7680

7681 gacaaggaaagaaggccagaggaatgtggaaagatgagcgaggacaggtgtggaggtttt 7740  
 . 7700 . 7720 . 7740

7741 gggctagctcttagtcttctgggtgtgagagagggattaaagtgccttatgcgcaagaatg 7800  
 . 7760 . 7780 . 7800

7801 tgtcaacaacaggtgttctctgccctctgctggcatgagttaggtgtggcttgggctgaatc . 7860  
 . . 7820 . 7840 . 7860

7861 caaatgtgtattggcacaagatggaaagcaaagtgtgctggagttactgggtgggagacag 7920  
 . 7880 . 7900 . 7920

7921 ggatgtatgtgggtcccccgctgggatgccagtaacctgtggaagtaagggggcctcatctg 7980  
 . 7940 . 7960 . 7980

7981 cctggtagttgtgttggtgcagaggtctgatgtgtgtaggaggggtgggttcaacgcaggg 8040  
 . 8000 . 8020 . 8040

8041 gcgttggtggcgagtcctggcaacgcccgggtccttgctacctgtgtggtgtgttaaggg 8100  
 . 8060 . 8080 . 8100

8101 ctgggtaaagggtgtctgccaattctctgcgatgtcctcctttcccttgttttgaaatagaa 8160  
 . 8120 . 8140 . 8160

8161 tatgaatgtggccttttcagcctagacagacagtgtggctaaggaggagtgtgtgccagttaa 8220  
 . . . . .  
 8180 . 8200 . 8220

8221 ggtgattagctaaggcattcccagtaaatggagggagagtcagtcaggccaagcctatgac 8280  
 . 8240 . 8260 . 8280

8281 atggtaatgcctagaagtaaagaaaggttagtcatagtagcttagctgaactgggccgtg 8340  
 . 8300 . 8320 . 8340

8341 ggggtcgtcatcatctccaccggaaccagaagaacccaaaagcagcgtaggaagggtgtgg 8400  
 . 8360 . 8380 . 8400

8401 atcaccgcccgcgatggccggaatcatgactatgaccgcccgcctccgtctgtcatcaaagg 8460  
 . 8420 . 8440 . 8460

8461 cgggcccttggtcacctcctttgttttcaacctcttcggtcaattgtggagggcctccatc 8520  
 . 8480 . 8500 . 8520

8521 atttccagcagagtcgctagggcctatgaggcagcgggtcatgtgggccattgtcatcagt 8580  
 . 8540 . 8560 . 8580

8581 gttgtcagggtcctctgtggggccattgtcatcagtggttgtcagggtcctgaggcagcgggtc 8640  
 . 8600 . 8620 . 8640

8641 atgtggggccattgtcatcagtggttgtcagggctcctgtggggccattgtcatcagtggttgtc 8700  
 . 8660 . 8680 . 8700

8701 agggctcctgtggggccattgtcaggaccacctccaggtgcgcctagggttttgagagcagag 8760  
 . 8720 . 8740 . 8760

8761 tgggggtccgctcgccggctccactcacgagcaggtggtgtctgccctcgttggagttaga 8820  
 . 8780 . 8800 . 8820

8821 gtcagattcatg gccagaatcatcggtagcttg ttgagggtgcgggagggagtcatcgtg 8880  
 . . 8840 . 8860 . 8880

8881 gtgggtgttcatactgtgtcgttgtccatggtaatacatccagattaaaatcgccagaaa 8940  
 . 8900 . 8920 . 8940

8941 caggaggagccaaaggagatcaaccaatagagtccaccagttttgttgtagatagagagc 9000  
 . 8960 . 8980 . 9000

9001 aataatgagcaggatgaggtctaggaagaaggctaggaagaaggccaaaagctgccagat 9060  
 . 9020 . 9040 . 9060

9061 ggtggcaccaagtcgccagagcatctccaataagtagatccagatacctaagactgcgtt 9120  
 . 9080 . 9100 . 9120

9121 gaaaaaaagagtgttaggggttgaaaaagtgggggtgtggtaaataattcctaggggaatgtt 9180  
 . 9140 . 9160 . 9180

9743 gggat===== 9747

360 380 400

345 ccctccggcctacttttggttgccgggctcttttgccccccctccaccgtgcttccttac 404

=====

420

405 tacggattcccacttgccgg----- 424

9748 =====ttgccccgggtctgccccggaggcagtagccgggtacagatttcccgaagcg 9794

9760 9780

-----

9795 gccgtgtgtgtgtgcatgtaagcgtagaaaggggaagtagaaagcgtgtgtttgtgttag 9854

9800 9820 9840

440 460 480

425 cagactacgtccccg-ctccctcgcgatccaacaagcgg-aaaagagacccccgaggagga 482

9855 aaaagcgggtccccgggggcaagctgtggga=atgcggtggccaagtgcacaggga=aa 9912

9860 9880 9900

500 520 540

483 tgaagaagcgccgggggctat-tccccggggaggacgccaccctctaccgcaaggacatag 541

9913 tggaaaggcagtgccggcaatcagaagggggag===== 9944

9920 9940

560 580 600

542 cgggcctctccaagagtgtgaatgagttacagcacacgctacaggccctgcgcggggaga 601

=====

620 640 660

602 cgctgtcctacggccacaccggagtcggatactgccccagcaggggcccctgctacaccc 661

=====

680 700 720

662 actcggggccttacggatttcagcctcatcaaagctacgaagtgccagatacgtccctc 721

=====

740 760 780

722 atccgccccaccaccaacttctcaccaggcagctcaggcgcagcctccacccccgggca 781

9945 =====tgcgtagtgttggtgggaagcggcagtgtaatctgcaca 9982

9960 9980

800 820

782 cacaggcccccgaaagccactgtgtggccgagtcacgatccctgaggcgggag----- 835

9983 aagaggcgccggggcgcaacgt=tgggag=gtcggtg=gccggcaggcgggaggccgtg 10038

10000 10020

-----

10039 ctttaggggggttcagggtgaggcaaggctgtggggtaaccgtaggggaggcgggtgaggc 10098

10040 10060 10080

840

836 -----cagccgggaa-ctc 848

10099 ggctaagagggttaagggtcgccgggtgacgaagcagcagacggcggatatgggaatttc 10158

10100 10120 10140

860 880 900

849 tggacccccg-ggaggacaccaaccctca-gcagccac-caccgag-ggc--ca-cca-c 900

10159 agaatgaggtggcggattcaggcgaaaagggtgtgggctgtgcgagtgatgagggcagg 10218

10160 10180 10200

```

          920          940          960
901  cgcggaaagaaactgggtgcaggcctctgcgtccggagtggtcagtcctaaggagcccacc 960
    ||||| |xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
10219 cgcggaaagtcgctgcggccttgctggggcatggggggccgcgcattcctggaaaaagtgg 10278
    10220          10240          10260
          980          1000          1020
961  accccaaggccaagtctgtgtcagcccacctaagtccatcttttgcgaggaattgctg 1020
    xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
10279 agggggcgtggccttcccccgcgccccccagccccccgcacagagcggcgctacggcg 10338
    10280          10300          10320

1021  aataaacgctggcttga----- 1038
    xxxxxxxxxxxxxxxxxxxxxxx
10339 ggcggggcggcggggggtcggggtccgcggggtccgggggctgcgggcggtggatggcggc 10398
    10340          10360          10380

-----

10399 ggacgttccggggatcgggggggtcggggggcgccgcgcggggcgagccatgcgtgaccg 10458
    10400          10420          10440

-----

10459 tgatgagggggcagggtcgcagggggtgtgtctggtgggggcgggagcggggggcgggcg 10518
    10460          10480          10500

-----

10519 gggagcctgcacgccgttgagggtagaatgacagggggcggggacagagaggcggtcgc 10578
    10520          10540          10560

-----

10579 gcccccgccgcgccagccaagcccccaagggggcggggagcgggcaatggagcgtgac 10638
    10580          10600          10620

-----

10639 gaaggggccccagggtgacccccggcaaactgacccggggctccggggtgaccagccaa 10698
    10640          10660          10680

-----

10699 gcgtgaccaagggggcccggtgggtgacacaggcaaccctgacaaaggccccccaggaaaga 10758
    10700          10720          10740

-----

10759 cccccggggggcatcgggggggtggggcatggggggccgcgcattcctggaaaaagtggag 10818
    10760          10780          10800

-----

10819 ggggcgtggccttcccccgcgccccccagccccccgcacagagcggcgctacggcggg 10878
    10820          10840          10860

-----

10879 cgggcggcgggggggtcgggggtccgcggggtccgggggctgcgggcggtggatggcggcg 10938
    10880          10900          10920

-----

10939 acgttccggggatcgggggggtcggggggcgccgcgcggggcgagccatgcgtgaccgtg 10998
    10940          10960          10980

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-----  
10999 atgagggggcaggggtcgcaggggggtgtgtctgtgtggggggcgggagcggggggcggcgcgg 11058  
11000 . 11020 . 11040 .

-----  
11059 gagcctgcacgccgttgagggttagaatgacagggggcggggacagagaggcggtcgcgc 11118  
11060 . 11080 . 11100 .

-----  
11119 ccccgccgcgccagccaagcccccaagggggggcggggagcgggcaatggagcgtgacga 11178  
11120 . 11140 . 11160 .

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11179 agggccccaggggtgaccccggaacacgtgacccggggctccgggggtgacccagccaagc 11238  
11180 . 11200 . 11220 .

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11239 gtgaccaagggggcccggtgggtgacacaggcaaccctgacaaaggccccccaggaaagacc 11298  
11240 . 11260 . 11280 .

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11299 cccgtggggcatggggggccgcgcattcctggaaaaagtggagggggcgtggccttcccc 11358  
11300 . 11320 . 11340 .

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11359 cgcggccccccagccccccgcacagagcggcgctacggcgggcggcgggcggggggtcg 11418  
11360 . 11380 . 11400 .

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11419 ggggtccgcgggctccggggggtgcgggcgggtggatggcgggcgacgttccggggatcggg 11478  
11420 . 11440 . 11460 .

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11479 ggggtcggggggcgccgcgcggggcgcagccatgcgtgaccgtgatgagggggcagggtcg 11538  
11480 . 11500 . 11520 .

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11539 caggggggtgtgtctgtgtggggggcgggagcggggggcggcgggagccctgcacgccgttg 11598  
11540 . 11560 . 11580 .

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11599 gagggtagaatgacagggggcggggacagagaggcggtcgcgcccccgccgcgccagcc 11658  
11600 . 11620 . 11640 .

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11659 aagcccccaagggggggcggggagcgggcaatggagcgtgacgaagggccccagggctgac 11718  
11660 . 11680 . 11700 .

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11719 cccggcaaacgtgacccggggctccgggggtgacccagccaagcgtgaccaagggggcccg 11778  
11720 . 11740 . 11760 .

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 11779 ggggtgacacaggcaaccctgacaaaggccccccaggaaagacccccggggggcatcgggg 11838  
 11780 . 11800 . 11820

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 11839 ggtggggcatggggggccgcgcattcctggaaaaagtggagggggcggtggccttcccccg 11898  
 11840 . 11860 . 11880

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 11899 cgccccccagccccccgcacagagcggcgctacggcgggcgggcggcggggggtcggg 11958  
 11900 . 11920 . 11940

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 11959 gtccgcggggtccgggggctgcgggcgggtggatggcggcgacgttcgggggatcggggg 12018  
 11960 . 11980 . 12000

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 12019 ggtcggggggcgccgcgcgggcgcagccatgcgtgaccgtgatgagggggcagggtcgca 12078  
 12020 . 12040 . 12060

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 12079 gggggtgtgtctggtgggggcgggagcggggggcggcgcgggagcctgcacgccgttgga 12138  
 12080 . 12100 . 12120

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 12139 gggtagaatgacagggggcggggacagagaggcggtcgcgcccccgccgcgccagccaa 12198  
 12140 . 12160 . 12180

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 12199 gcccccaagggggcggggagcgggcaatggagcgtgacgaagggccccagggtgacct 12258  
 12200 . 12220 . 12240

-----  
 12259 cggcaaacgtgaccgggggtccgggggtgaccagccaagcgtgaccaagggggcccgtgg 12318  
 12260 . 12280 . 12300

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 12319 gtgacacaggcaaccctgacaaaggccccccaggaaagacccccggggggcatcgggggg 12378  
 12320 . 12340 . 12360

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 12379 ggtgttgcgggggcatgggggggtcggtatttcgccttattgccctgtttagaattc 12436  
 12380 . 12400 . 12420

% Identity = 1.6 (210/12958)

///

9310-13DVCTDV SEQ ID NO 3.xdna x Bankier et al. EcoRI Dhet fragment complement.xdna => DNA Parallel

DNA sequence 1038 bp atgctatcaggt ... cgcgtggcttga linear

DNA sequence 12436 bp gaattctaaaca ... ctttgagaattc linear

Method: Blocks (Martinez)  
Layout: Standard  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Translation: Off

Alignment 10. Comparison of nucleotide sequence  
of SEQ ID NO:3 with the complement of the  
nucleotide sequence of Fig. 2 of Bankier et al.

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1  gaattctaaacagggcaataagggcgaaatccgaccccccatgccccgccaacacccc 60
    .                20                .                40                .                60
-----
61  ccccgatgcccccggggtctttcctggggggcctttgtcaggggttgctgtgtcacccc 120
    .                80                .                100               .                120
-----
121 acgggccccttggtcacgcttggtgggtcaccccgagccccgggtcacgtttgccggg 180
    .                140               .                160               .                180
-----
181 gtcagccctggggcccttcgtcacgctccattgcccgctccccgcccccttgggggctt 240
    .                200               .                220               .                240
-----
241 ggctggcgcgggccgggggcgcgaccgcctctctgtccccgccccctgtcattctaccctc 300
    .                260               .                280               .                300
-----
301 caacggcgtgcagggtccccgcgcgcccccccgctccccgccccaccagacacaccccctg 360
    .                320               .                340               .                360
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361 cgaccctgccccctcatcacgggtcacgcatgggtgcgcgcgcggcgccccccgacccc 420
    .                380               .                400               .                420
-----
421 cccgatcccccggaacgtccgcccgcaccccgcccgagcccccgagccccgaggaccc 480
    .                440               .                460               .                480
-----
481 cgaccccccgccgcccgcgcgtagcgccgctctgtgcgggggggctggggggcgccgcg 540
    .                500               .                520               .                540
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541 ggggaaggccacgccccctccactttttccaggaatgcgcggccccccatgccccacccc 600
    .                560               .                580               .                600

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1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	

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1321 gcgaccgcctctctgtccccgccccctgtcattotacctccaacggcggtgcaggctccc 1380  
 . 1340 . 1360 . 1380

1381 gcgcccgcggcgctccgcggcaccagacacacccccctgcgaccctgcccccctcatca 1440  
                  .                    .                    .  
                        1400                        1420                        1440

1441 cggtcacgcgatggctgcgcccgcgcgggcgcccccgacccccgatccccggaacgtcc 1500  
 . 1460 . 1480 . 1500

1501 gccgccatccaccgcccgcagccccggagcccgcggaccccgacccccgcgcgccgcc 1560  
 . 1520 . 1540 . 1560

1561 cgccgtagcgccgctctgtgcgggggggctggggggccgcgggggaaggccacgccccct 1620  
 . 1580 . 1600 . 1620

1621 ccactttttccaggaatgcgcggccccccatgccccacccccgatgccccccgggggtc 1680  
 . . 1640 . 1660 . 1680

1681 tttcctggggggcctttgtcagggttgcctgtgtcacccacggggccccttgggtcacgctt 1740  
 . . 1700 . 1720 . 1740

1741 ggctgggtcaccocggagccocgggtcacgtttgccgggggtcagccctggggcccttcgt 1800  
 . 1760 . 1780 . 1800

1801 c a c g c t c c a t t g c c c g c t c c c c g c c c c c c t t g g g g g c t t g g c t g g c g c g g c g g g g g c g c 1860  
 . 1820 . 1840 . 1860

1861 gaccgcctctctgtccccgccccctgtcattctaccctccaacggcgtgcaggctccgc 1920  
 . 1880 . 1900 . 1920

1921 gccgccccccgctcccgccccaccagacacaccccctgcgaccctgccccctcatcacg 1980  
 . 1940 . 1960 . 1980

1981 gtcacgcatggctgcgcccgcgcgccccgacccccgatccccggaacgtccgc 2040  
 . 2000 . 2020 . 2040

2041 cgccatccaccgcccgcagccccggagcccgcgaccccgacccccgccgcccgcgg 2100  
 . 2060 . 2080 . 2100

2101 ccgtagcgcgcgctctgtgcgggggggctggggggccgcgggggaaggccacgccccctcc 2160  
 . 2120 . 2140 . 2160

2161 actttttccaggaatgcgcggcccccattgcccagcaagccgcagcgacttttcgcgcgc 2220  
 . 2180 . 2200 . 2220

2221 tgcctcatgacactcgcacagccacaccccttttcgcctgaatccgccacctcattctga 2280  
 . 2240 . 2260 . 2280

2281 aattcccataatccgcgcgtctgctgcttgcgcacccgcgcgaccttagccctcttagccgc 2340  
 . 2300 . 2320 . 2340

2341 ctcacccgcctccctacggttaccacacagccttgccctcacctgaacccccctaaagca 2400  
 . 2360 . 2380 . 2400

2401 cggcctcccgccctgccgccaacgacctccaacgttgcgcgccccgcgcctctttgtgca 2460  
 . 2420 . 2440 . 2460

2461 gattacactgccgcttcccacaacactacgcactcccccttctgattgccgcactgcctt 2520  
 . 2480 . 2500 . 2520

2521 tccatttctctgttgcaacttggccaccgcattcccacagcttgccccccggggaccgcgtt 2580  
 . 2540 . 2560 . 2580

2581 ttctaacacaaacacacagcttttctacttccccctttctacgcttacatgcacacacacacc 2640  
 . 2600 . 2620 . 2640

2641 gccgccttttcgggaaatctgtaccgcgtactgcctccggcagaccccgcaaatcccccggg 2700  
 . 2660 . 2680 . 2700

2701 cctacatcccaagaaacacgcgttactctgacgtagccgccctacataagcctctcacac 2760  
 . 2720 . 2740 . 2760

2761 tgctctgcccccttcttttctcaactgccttgctcctgacacactgccttgaggatggaa 2820  
 . 2780 . 2800 . 2820

2821 cacgaccttgagagggggccaccggggccgcgacggccccctcgaggacccccctctcc 2880  
 . 2840 . 2860 . 2880

2881 tcttccctaggccttgctctctcttctctctcttggcgctactgttttggtgtacatc 2940  
 . 2900 . 2920 . 2940

2941 gttatgagtgactggactggaggagccctccttgtcctctattcctttgctctcatgctt 3000  
 . 2960 . 2980 . 3000

3001 ataattataat<sup>ttt</sup>gatcatct<sup>t</sup>tatatcttcagaagagac<sup>tt</sup>tctctgtccacttg<sup>g</sup>agcc 3060  
                  .<sup>.</sup>                    3020                      .<sup>.</sup>                    3040                      .<sup>.</sup>                    3060

3061 ctttgtatactcctactgatgagtaagtattacaccctttgccccacacccccctttccct 3120  
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 . 3200 . 3220 . 3240

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 . 3260 . 3280 . 3300

3301 ctaacactcttttttcaacgcagtccttaggtatctggatctacttattggagatgctctg 3360  
 . 3320 . 3340 . 3360

3361 gcgacttggtgccaccatctgtgcagcttttggcctttcttctagccttcttcttagacct 3420  
 . 3380 . 3400 .. 3420

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 . 3440 . 3460 . 3480

3481 cctttggctcctcctgtttctggcgattttaatctggatgtattaccatggacaacgaca 3540  
 . 3500 . 3520 . 3540

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 . 3560 . 3580 . 3600

3601 tggccatgaatctgactctaactccaacgagggcagacaccacctgctcgtgagtggagc 3660  
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 . 3680 . 3700 . 3720

3721 tggccacaggaccctgacaacactgatgacaatggccacaggaccctgacaacactga 3780  
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 . . . . . 3920 . . . . . 3940 . . . . . 3960

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4381 actccgccaccaacgcccctgcgttgaaacccacccctcctacacacatcagacctctgca 4440  
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4441 caacacaactaccaggcagatgaggcccttacttccacagggtagtggcataccagcgg 4500  
 . 4460 . 4480 . 4500



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1970 1971 1972 1973 1974 1975 1976 1977 1978 1979 1980 1981 1982 1983 1984 1985 1986 1987 1988 1989 1990 1991 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 2011 2012 2013 2014 2015 2016 2017 2018 2019 2020

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21 -----agaaggagc----- 29

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5221 cagcgcctgggggtgtcaacaaagaactttgacctgttgccctgagatgtgaattgggat 5280  
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5341 taaataaaaagtacagatagatggcactcttaccttcctctgcccgcttcttcgtatatgt 5400  
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5641 gggagttgtttccgccatcgtacccatccggatccccgccggggctagggggaccgcgc 5700  
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 . 5720 . 5740 . 5760

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 . 5780 . 5800 . 5820

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                    5840                    5860                    5880

5881 ttcttgagagcccaggggtctctgtgcagggtgtccccggggaattgttctccctgatcacc 5940  
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 . 6020 . 6040 . 6060

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      6080               6100               6120
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6121 tattgcgacaagtatccagaaacataaaccccggtgggcttcctccttgtcatttttccca 6180
      .               .               .               .
      6140               6160               6180
30 -----aacag----- 34
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6181 acgcaggtcactggcaggtgccagggcttgggaagtgcaggtcaacagcaacagagagg 6240
      .               .               .               .
      6200               6220               6240
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      6260               6280               6300
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6301 tcgggcatgagccactggacgtggggatggggaaatgcattcacggtgcatgtcacagta 6360
      .               .               .               .
      6320               6340               6360
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6361 aggacagagaagtctggaactgagaccttctcgagtgagacagacagcgtagaggcttc 6420
      .               .               .               .
      6380               6400               6420
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      .               .               .               .
      6440               6460               6480
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6481 tagttgccgtcatgggagatggtggcagcggtgactactaaaaagaaggtggtggcaatt 6540
      .               .               .               .
      6500               6520               6540
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      .               .               .               .
      6560               6580               6600
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6601 cgcccaataagcacctgctcctctcctggggccagtttaaacagctgacctcaatctct 6660
      .               .               .               .
      6620               6640               6660
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      .               .               .               .
      6680               6700               6720
35 -----cctg----- 38
      |||||
6721 gtgacagcctggcgggcgccacacaggaggccaacaggaggagctgagcgatgaacctg 6780
      .               .               .               .
      6740               6760               6780
-----
6781 gccattgctctggactctcctcaccagggcctcgcgctttatactattctgccacgccc 6840
      .               .               .               .
      6800               6820               6840

```

6841 ttttatcatataagcctgaagcccgtagctggcctgacgagaccatgaggccagccaag 6900  
 . 6860 . 6880 . 6900

6901 tctacagattctgtgtttgtgaggacccccggtcgaggcggtgggtcgcgccctcgccgcgcg 6960  
 . 6920 . 6940 . 6960

6961 gacgacaaggtggctgagtcacgctacctcatgttcagggccatgtacgcggtgttcacc 7020  
 . 6980 . 7000 . 7020

7021 cgggatgagaaagacctgcctttgccagccctggctctctgccggctcatcaaggcctcc 7080  
 . 7040 . 7060 . 7080

39 -----cggagggt 45  
 ||||  
 7081 ctgaggaaggataggaagctgtacgcggagctggcctgcaggacagccgacatcgggggc 7140  
 . 7100 . 7120 . 7140

46 tcggccgcccgcgggccaggacctcatcagcgctccccgcgaacacctttatgaca----- 99  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
7141 aaagacacgcacgtacggctcatcattcagcgctcctgcgcgcagtgtacaacgaccactac 7200  
          .               7160                    .               7180                    .               7200

7201 gactactggtcgcggtcaggggtggtgctgtgctacacagtgggtgtttgcgggtgcgaac 7260  
 . 7220 . 7240 . 7260

7261 tacctggatgaccacaagagcgccgccttcgtgctgggggcaatcgcccactacctggcc 7320  
 . 7280 . 7300 . 7320

7321 ctctatcgcagactctggtttgcgaggctgggcggcatgccaaagatcgctgagacgtcag 7380  
 . 7340 . 7360 . 7380

7381 ttccccgtgacgtgggccctggccagcctgactgacttcttgaatatctttgtaaatgaat 7440  
 . 7400 . 7420 . 7440

7441 aaacagtgggtgttcgctgatgagtaaagtgtaacatttaatgtgggactgggaggccgg 7500  
 . 7460 . 7480 . 7500

7501 ggcgataccttgggcatcatgcagggtgcacagactagcgaggataatctgggcagccag 7560  
 . 7520 . 7540 . 7560

7561 agccagccgggtccgtgcggtacatctacttttaccacctggccacctacctcttagg 7620  
 . 7580 . 7600 . 7620

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8341 agcgcggcatgcgagctggcggtgagctacgcacccgccatgctggaggcctcgcacgag 8400  
 . 8360 . 8380 . 8400

9121 ctggagcggctgtctcggctgggcatagacgctgaaggaaagctagagaaggagccccat 9180  
 . 9140 . 9160 . 9180

9181 ggccgcgctgactttgtcaagatgttcaaggacgtggatgcgcggtggacgccgaagtg 9240  
 . 9200 . 9220 . 9240

9241 gtccagttttatgaacagcatggccaagaacaacatcacctacaaggacctgggtcaagagc 9300  
 . 9260 . 9280 . 9300

9301 tgctaccacgtgatgcagtactcgtgcaacccctttgcgcagcccgccctgccccatcttc 9360  
 . . . . . 9320 . . . . . 9340 . . . . . 9360

9361 acccagctgtttttaccgctcactgctgaccatcctgcaggacatctccctgcccatctgt 9420  
 . 9380 . 9400 . 9420

9421 atgtgctatgagaatgacaacccgggcttgccagagccccccagagtggctaaaggggt 9480  
 . 9440 . 9460 . 9480

9481 cactaccagacgctgtgcaccaacttttaggagcctggccatcgacaagggggtcctcacg 9540  
 9500 9520 9540

9541 gccaaaggaggccaaggtggtgcatggggagcccacctgcgacctgccagacctggacgcg 9600  
 . 9560 . 9580 . 9600

9601 gccctgcagggccgggtgtacggccggcggtgcctgtgcgcattgtccaaggtgctgatg 9660  
 . 9620 . 9640 . 9660

9661 ctgtgccccaggaacatcaagatcaagaacaggggtggttttcacgggggagaatgccgcc 9720  
 . 9680 . 9700 . 9720

9721 ctccagaacagcttcacgaagtcactaccaggaggaggagaactacatcatcaacggggccc 9780  
 . 9740 . 9760 . 9780

9781 tacatgaaattcctcaacacctaccacaagaccctattccggacactaagctctcaagc 9840  
 . 9800 . 9820 . 9840

9841 ctgtacctgtgggcacaaacttttccaggcgggcgctcggtccctgtccccagcgggggccagc 9900  
 . 9860 . 9880 . 9900

9901 gcggaggagtactctgacctggccctctttgtggacgggggctcccgggccacgaagag 9960  
 . . . . . 9920 . . . . . 9940 . . . . . 9960

9961 agcaacgtcatagatgtgggtgacctggcaacctgggtcacttacgccaaagcagaggctcaac 10020  
 . 9980 . 10000 . 10020

10021 aacgccatcctgaaggcgtgcggccagaccagttctacatcagcctgattcagggactg 10080  
 . 10040 . 10060 . 10080

10081 gtgccgaggacgcagtcggtgcccgcccgtgactacccccacgtactgggcacgcgggcg 10140  
 . 10100 . 10120 . 10140

```

149 -----cctacgcgg----- 157
          |||||
10141 gtggagtcggcagcggcctacgcggaggccacctcctcccttactgcgaccacggtggtc 10200
          .      10160      .      10180      .      10200

```

158 -----ccccgctgcc 168  
                  | |||||x  
10201 tgcgcggccacagactgtcttagccagggtctgcaaggcccggtcggttgtcacgctgcca 10260  
                       10220                       10240                       10260

169 cccttttccaccagg----- 184  
xxxxxxxxxxxxxxxxxx  
10261 gtgaccatcaacaagtacacgggggtcaacggcaacaaccagatatccaggcggggaac 10320  
                  10280                  10300                  10320

10321 ctgggatactttatggggcggggcggtggacaggaacctgctgcaggcccccggggctggg 10380  
 . 10340 . 10360 . 10380

10381 ctgcgcaagcaggccgggggctcttccatgcggaagaagtttgctttgccacccccacc 10440  
 . 10400 . 10420 . 10440

10441 ctagggttgaccgtgaagcgccgggacccaagccgcgaccacatatgagattgagaacatc 10500  
 . 10460 . 10480 . 10500

10501 agggctggcctggaggccattatatcacaaaaacaggaggaagactgtgtgtttgatgtg 10560  
 . 10520 . 10540 . 10560

10561 gtgtgcaaccttgttgatgccatgggagaggcatgcgcctcgctgactagggacgacgcg 10620  
 . 10580 . 10600 . 10620

10621 gagtacttattggggcgcttctccgtcctggcggaacagcgtcctagaaaccctggcgacc 10680  
 . . 10640 . 10660 . 10680

10681 attgcctccagcgggatagagtggacggcggaggccgctcgggactttctggagggagtg 10740  
 . 10700 . 10720 . 10740



10741 tgggggtgggcccggggcagcccagcacaactttatcagcgtggccgagccggtcagcacc 10800  
 . 10760 . 10780 . 10800

10801 gcgtcgcaggcctcgccgggctgctgctgggtggaggaggcagggctccgggggcaga 10860  
 . 10820 . 10840 . 10860

10861 cgcaagcgccgtctggccaccgttctccccggactcgaggtctagagaccctggggcg 10920  
 . 10880 . 10900 . 10920

10921 cgatgtcggggctgctggcggcggcgtacagccaggtgtacgccctggcggttgagctga 10980  
 . 10940 . 10960 . 10980

10981 gcgtgtgcaccggctggaccccgagtgctggacgtggctgcggtggtgcgcaacgccg 11040  
 . 11000 . 11020 . 11040

11041 gcctgctggccgagctggaggccatcctccttccccgtttgagacggcagaatgaccgtg 11100  
 . 11060 . 11080 . 11100

11101 catgcagcgcacctgtccctggagctggtgcacctgctagagaactcgagagaggcctctg 11160  
 . 11120 . 11140 . 11160

11161 ccgcgctgctcgcccctggtagaaagggtacccgggtcccgccctctccgtacccctcag 11220  
 . 11180 . 11200 . 11220

11221 tcgcgtactctgtggagttttacggggggcataaagtcgatgtaagtttgtgcctaataa 11280  
 . 11240 . 11260 . 11280

185 -----caatagc----- 191

11281 atgacatagagattttaatgaagagaatcaatagcgtgtttttattgcatgtctcacacca 11340  
 . 11300 . 11320 . 11340

11341 tggggctggagagcctggaacgggccctggatctgctgggccgctttcggggcgtaagtc 11400  
 . 11360 . 11380 . 11400

11401 ccattcccagaccgcgcctctacatcacctctgtgcccctgctggcgctgtgtgggcgagc 11460  
 . 11420 . 11440 . 11460

11461 tgatggttctgcccaaccacggcaacccttcacggcagaggggaccacgtctcctgta 11520  
 . 11480 . 11500 . 11520

11521 accacctggcggtgccggtgaatccggagccggtctcgggactgtttgagaatgaagtcc 11580  
 . 11540 . 11560 . 11580

11581 gccaggcggggctcgggcacctgttgaggctgaggagaaggcgaggccgggcggccag 11640  
 . 11600 . 11620 . 11640

192 --caccgcgccttccctacgggtcctgg-ggccgag----- 223  
      |          |||     |     |     |     |  
 11641 aggaggcgcggtcccggggcccgggcgggccgagggcagagggggcgaccagagcgctgg 11700  
                 11660                    11680                    11700

11701 acacctacaacgtcttctcgcacagtgcggcgagggtggcgagctctcggagctcctct 11760  
 . 11720 . 11740 . 11760

11761 attggaactctggcgccatgctatcggtgcaacggggcagggggaggggtggcgccatt 11820  
 . 11780 . 11800 . 11820

11821 cccgcctctctgccctgtttgcccgaggcgctgcctggccctggtgcgggggacctgcg 11880  
 . 11840 . 11860 . 11880

11881 aggaggcgctggcgggggcaaggctgactcacctgtttgacgccgtggctcccggggcca 11940  
 . 11900 . 11920 . 11940

224 -----cgg-tc----- 228  
 ||| ||  
 11941 cggagcggctcttctgcgggcggggtctacagctcctcgggcgacgcggtggaggcgctga 12000  
 . 11960 . 11980 . 12000

12001 aggcggactgcgcgcgcgcttcacggcgacccccagtaccggggccatcctgcaaaaga 12060  
 . 12020 . 12040 . 12060

12061 ggaacgagctgtacacgcggctcaaccgagccatgcagcggttgggccgaggcgaggagg 12120  
 . 12080 . 12100 . 12120

229 -----gccccggccggcggtactttacctccccaggagg 263

12121 aggcgtcccgaggagagcccggaggtgccccggccggc===== 12157  
          .  
               12140                .

264 ttactacgccgggcccgcgggcggggacccgggtgccttcttggcgatggacgctcacac 323

324 ctaccacccccaccacacccccctccggcctactttggccttgcgcgggcctcttttggccc 383

```

      400      420      440
384 ccctccaccgtgcctccttactacggattcccacttgcgggcagactacgtccccgctcc 443
=====

      460      480      500
444 ctcgcgatccaacaagcggaaaagagacccccgaggagatgaagaaggcggggggctatt 503
      ||| ||| ||| ||| ||| ||| |||
12158 =====tggggcacg=agagcccggcccggtccgg 12184
      12160      12180
      520      540      560
504 cccgggggaggacgccaccctctaccgcaaggacatagcgggcctctccaagagtgtgaa 563
      ||| ||| ||| ||| ||| ||| |||
12185 cgccctctcggacg==cgctcaagcgcaagga===== 12214
      12200
      580      600      620
564 tgagttacagcacacgctacaggccctgcgcgggagacgctgtcctacggccacaccgg 623
      ||| ||| ||| ||| ||| ||| |||
12215 =====gcagtacctgcgcaggtgg===== 12234
      12220
      640      660      680
624 agtcggatactgccccagcagggccctgctacaccactcggggccttacggatttca 683
=====

      700      720      740
684 gcctcatcaaagctacgaagtgccagatacgtccctcatccgccccaccaccaacttc 743
=====

      760      780      800
744 tcaccaggcagctcaggcgcagcctccacccccgggcacacaggccccgaagccactg 803
=====

      820      840      860
804 tgtggccgagtcacagatccctgaggcgggagcagccgggaactctggacccccgggagga 863
=====

      880      900      920
864 caccaaccctcagcagcccaccaccgagggccaccaccgcggaaagaaactggtgcaggc 923
      ||| ||| ||| ||| ||| ||| |||
12235 =====ccaccgaggggtct===== 12247
      12240
      940      960      980
924 ctctgcgtccggagtggctcagtctaaggagcccaccaccccccaaggccaagtctgtgtc 983
      ||| ||| ||| ||| ||| ||| |||
12248 =====ggccaagctgcagtc 12262
      12260
      1000      1020
984 a-gcccacctcaa--gtcc-atcttttgcgag-gaattgctgaataaacgcgtggcttga 1038
      ||| ||| ||| ||| ||| ||| |||
12263 ctgcctggcgcaacagagcgagaccctgaccgagaccctgtgcctgcgcgtctgggggga 12322
      12280      12300      12320
-----

12323 cgtggtctactgggagctggcccgcatgcgcaaccacttccctctacagacgggccttcgt 12382
      12340      12360      12380
-----

12383 ctcggggtccctgggaggacaggcgcgccggcgagggtgccgcctttgagaattc 12436
      12400      12420

```

% Identity = 1.8 (239/13074)

9310-13DVCTDV SEQ ID NO 3.xdna x Bankier et al. EcoRI Dhet fragment/18/07/5-02/4-1PM=> DNA Parallel

///

9310-13DVCTDV SEQ ID NO 2.xprt x Bankier et al. BA-LF3.xprt => Protein Alignment

Protein sequence 177 aa MARRLPKPTLQG ... DTAPRGARKKQ\*

Protein sequence 609 aa \*GRRGVLIGPLL ... DRRAGEGAAAFEN

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 11.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:1 (SEQ ID NO:2) with the amino acid sequence, BA-LF3, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .           20           .           40           .           60
1  MARRLPKPTLQGRLEADFPDSPLLPKFQELNQNNLPNDVVFREAQRSYLVFLTSQFCYEEY 60
      RR           R           P +P           Q           +           Q Y+
1  *GRRGVLIGPLLRRPGGQRP RNP GDHCLQRDRVDGGGRSGLSGGSVGVWARGSPGQL=YQRG 59
      .           20           .           40           .           60
61 VQRTFGVPRRQRAIDKRQ RASVAGAGAHHLGGSSATPVQQAQAAASAGTGALASSAPST 120
      V           RA           +RA + G           S T           + AA +G A A S
60 RAGQHRVAGLGRAGAAAGWRRAGLRGQTQAPSGHRSPRTRGLETPGAAMSGLLAAAYSQVYA 119
60 .           80           .           100           .           120
121 -AVAQSATPSVSSSISSLRAATSGATAAASAAA VDTGSGGGGQPHDTAPRGARKKQ*-- 177
      AV S           +           + A           A A           A +           +A
120 LAVELSVCTRLDPRSLDVA AVVRNAGLLAELEAILLPRLRRQNDRACSALSLELVHLLN 179
120 .           140           .           160           .           180
-----
180 SREASAALLAPGRKGTRVPPLRTPSVAYSVEFYGGHKVDVSLCLINDIEILMKRINSVFY 239
180 .           200           .           220           .           240
-----
240 CMSHTMGLESLEALRDL LGRFRGVSPIDPRLYITSVPCWRCV GELMVLPNHGNPSTAEG 299
240 .           260           .           280           .           300
-----
300 THVSCNHLAVPVNPEPVSGLFENEVRQAGLGHLLEAEEKARPGGP EEGAVPGPGRPEAEG 359
300 .           320           .           340           .           360
-----
360 ATRALDTYNVVFSTVPPEVAELSEL LYWNSGGHAIGATGQGE GGGHSRLSALFARERRLAL 419
360 .           380           .           400           .           420
-----
420 VRGACEEALAGARLTHLFD AVAPGATERLFCGGVYSSSGDAVEALKADCAA AFTAHPQYR 479
420 .           440           .           460           .           480
-----
480 AILQKRNELYTRLN RAMQRLGRGEEEEASRESPEVPRPAGAREPGPSGALS DALKRKEQYL 539
480 .           500           .           520           .           540
-----
540 RQVATEGLAKLQSC LAQQSETLTETLCLRVWGDVVY WELARMRNHFLYRR AFVSGPWEDR 599
540 .           560           .           580           .           600

```

-----  
600 RAGEGAAFEN  
600

609

% Identity = 4.9 (30/610)      % Homology = 2.0 (12/610)      % Total = 6.9 (42/610)

///

9310-13DVCTDV SEQ ID NO 4.xprt x Bankier et al. BA-LF3.xprt => Protein Alignment

Protein sequence 346 aa MLSGNAGEGATA ... FCEEELNKRVA\*

Protein sequence 609 aa \*GRRGVLIGPLL ... DRRAGEGA AFEN

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 12.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:3 (SEQ ID NO:4) with the amino acid sequence, BA-LF3, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      20      40
1 MLSGNAGEGATAC-GGSAAAGQ-D--LIS--VPRNTFMTLLQTNLDNKP--PRQTPLPYA 52
      G      GG      D L      V      L      ++      P Q
1 *GRRGVLIGPLLRRPGGQRPRNPGDHCLQRDRVDGGGRSGLSGGSGVWARGSPGQLYQRGR 60
      20      40      60
53 APLPPFSHQAIATAPSYGPGAGAVAPAGGYFTSPGGYYAGPAGGDPGAFLAMDAHTYHPH 112
      A      +      A A      G      A      SP      G      LA      +
61 AGQHRVAGLGRAAAGWRRAGLRGQTQAPSGHRSPRTRGLETPGAAMSGLLAAAYSQVYAL 120
      80      100      120
113 PHPPPAYFGL-PG-LFGPPPPCLLTDSHLRADYVPAPSRSNKRKRDPDEEGGGLFPG 170
      L P L      + L A +P      R N R      E      L
121 AVELSVCTRLDPRSLDVAAVVRNAGLLAELEAILLPRLRRQNDRACSALSLELVHLLENS 180
      140      160      180
171 EDATLYRKDIAGLSKSVNELQHTLQALRRETLSYGHTGVGYCPQQGPCYTHSGPYGFQPH 230
      +A+      V L+      A E      V C
181 REASAALLAPGRKGTRVPPLRTPSVAYSVEFYGGHKVDVSLCLINDIEILMKRINSVFYC 240
      200      220      240
231 QSYEVPRYVPHPPPPPTSHQAAQAQPPPPG---TQAPEAHCVAESTI-PEAGAAGNS-GP 285
      S+ +      + P P      T P      CV E + P G      + G
241 MSHTMGLESLELALDLLGRFRGVSPIDPRLYITSVPCWRCVGLMVLNHNPNSTAEGT 300
      260      280      300
286 REDTNPQQ-PTTEGHHRGKKL--V-QASASGVAQSKEPTTPKAKSVSAHLKSIFCEELN 341
      N      P      G      V QA      + +++E      P      A      E
301 HVSCNHLAVPVNPEPVSGLFENEVRQAGLGHLLEAEAEKARPGGPPEGAVPGPGRPEAEGA 360
      320      340      360

342 KRVA*----- 346
      R
361 TRALDTYNVFSTVPPEVAELSELLYWNSSGGAIGATGQGE GGGHSRLSALFARERRLALV 420
      380      400      420

-----

421 RGACEEALAGARLTHLFDVAVPGATERLFCGGVYSSSGDAVEALKADCAAFTAHPQYRA 480
      440      460      480

-----

481 ILQKRNELYTRLNRAMQRLGRGEEEA SRESPEVPRPAGAREPGPSGALS DALKRKEQYLR 540
      500      520      540

-----

541 QVATEGLAKLQSCLAQQSETLTETLCLRVWGDVVYWE LARMRNHFLYRRAFVSGPWEDRR 600
      560      580      600

```

-----  
601 AGEGAAFEN

609

% Identity = 9.7 (59/609)

% Homology = 3.0 (18/609)

% Total = 12.6 (77/609)

///



9310-13DVCTDV SEQ ID NO 5.xprt x Bankier et al. BA-LF3.xprt => Protein Alignment

Protein sequence 24 aa AVDTGSGGGGQP ... HDTAPRGARKKQ  
 Protein sequence 609 aa \*GRRGVLLIGPLL ... DRRAGEGAAFEN

Method: Diagonals (BLOSUM62)  
 Layout: Standard  
 Block Length ≤: 6-aa  
 Mismatch penalty: Smaller (1)  
 Gap penalty: Medium (2)  
 Display: BLOSUM62

Alignment 13. Comparison of the amino acid sequence of  
 SEQ ID NO:5 with the amino acid sequence, BA-LF3, encoded  
 by the nucleotide sequence of Fig. 2 of Bankier et al.

```

-----
1 *GRRGVLLIGPLLPGGQRP RNP GDHCLQ RDRVDGGGRSGLSGGSVGVWARGSPGQLYQRGR 60
      .          20          .          40          .          60
-----
61 AGQHRVAGLGRAAAGWRRAGLRGQTQAPS GHRSPRTRGLETPGAAMSGLLAAAYSQVYAL 120
      .          80          .          100          .          120
-----
121 AVELSVCTRLDPRSLDVA AVVRNAGLLAELEAILLPRLRRQNDRACSALSLELVHLLENS 180
      .          140          .          160          .          180
-----
181 REASAALLAPGRKGTRVPPLRTPSVAYSVEFYGGHKVDVSLCLINDIEILMKRINSVFYC 240
      .          200          .          220          .          240
-----
241 MSHTMGLESLE RALDLLGRFRGVSPIPDPRLYITSVPCWRCV GELMVLPNHGNPSTAEGT 300
      .          260          .          280          .          300
-----
301 HVSCNHLAVPVNPEPVSGLFENEVRQAGLGHLLEAE EKARPGGP EEGAVPGPGRPEAEGA 360
      .          320          .          340          .          360
-----
361 TRALDTYNVFSTVPPEVAELSEL LYWNSGGHAIGATGQGE GGGHSRLSALFARERRLALV 420
      .          380          .          400          .          420
-----
421 RGACEEALAGARLTHLFD AVAPGATERLFCGGVYSSSGDAVEALKADCAA AFTAHPQYRA 480
      .          440          .          460          .          480
-----
481 ILQKRNELYTRLN RAMQRLGRGEEEEASRESPEVPRPAGAREPGPSGALS DALKRKEQYLR 540
      .          500          .          520          .          540
1 -----AVDTGSGGGGQP HDT 15
      .          G
541 QVATEGLAKLQSC LAQQSETLTETLCLRVWGDVVY WELARMRNHFLYRRAFVSGPWEDRR 600
      .          560          .          580          .          600
    
```

20  
16 APRGARKKQ  
A GA +  
601 AGEGAAFEN

24

609

% Identity = 0.7 (4/609)      % Homology = 0.2 (1/609)      % Total = 0.8 (5/609)

///

9310-13DVCTDV SEQ ID NO 6.xprt x Bankier et al. BA-LF3.xprt => Protein Alignment

Protein sequence 30 aa STAVAQSATPSV ... LRAATSGATAAA

Protein sequence 609 aa \*GRRGVLLIGPLL ... DRRAGEGAAFEN

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

Alignment 14. Comparison of the amino acid sequence of SEQ ID NO:6 with the amino acid sequence, BA-LF3, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

-----
1 *GRRGVLLIGPLL R P G G Q R P R N P G D H C L Q R D R V D G G G R S G L S G G S V G W A R G S P G Q L Y Q R G R 60
   .                20                .                40                .                60
-----
61 A G Q H R V A G L G R A A A G W R R A G L R G Q T Q A P S G H R S P R T R G L E T P G A A M S G L L A A A Y S Q V Y A L 120
   .                80                .                100                .                120
-----
121 A V E L S V C T R L D P R S L D V A A V V R N A G L L A E L E A I L L P R L R R Q N D R A C S A L S L E L V H L L E N S 180
   .                140                .                160                .                180
-----
181 R E A S A A L L A P G R K G T R V P P L R T P S V A Y S V E F Y G G H K V D V S L C L I N D I E I L M K R I N S V F Y C 240
   .                200                .                220                .                240
-----
241 M S H T M G L E S L E R A L D L L G R F R G V S P I P D P R L Y I T S V P C W R C V G E L M V L P N H G N P S T A E G T 300
   .                260                .                280                .                300
-----
301 H V S C N H L A V P V N P E P V S G L F E N E V R Q A G L G H L L E A E E K A R P G G P E E G A V P G P G R P E A E G A 360
   .                320                .                340                .                360
-----
361 T R A L D T Y N V F S T V P P E V A E L S E L L Y W N S G G H A I G A T G Q G E G G G H S R L S A L F A R E R R L A L V 420
   .                380                .                400                .                420
-----
421 R G A C E E A L A G A R L T H L F D A V A P G A T E R L F C G G V Y S S S G D A V E A L K A D C A A A F T A H P Q Y R A 480
   .                440                .                460                .                480
-----
481 I L Q K R N E L Y T R L N R A M Q R L G R G E E E A S R E S P E V P R P A G A R E P G P S G A L S D A L K R K E Q Y L R 540
   .                500                .                520                .                540
1 -----STAVAQSATPSVSSSISSLR 21
   .                20
541 Q V A T E G L A K L Q S C L A Q Q S E T L T E T L C L R V W G D V V Y W E L A R M R N H F L Y R R A F V S G P W E D R R 600
   .                560                .                580                .                600

```

22 ATSGATAAA  
A GA  
601 AGEGAAFEN

30

609

% Identity = 0.8 (5/609)

% Homology = 0.2 (1/609)

% Total = 1.0 (6/609)

///

9310-13DVCTDV SEQ ID NO 2.xprt x Bankier et al. BA-LF2.xprt => Protein Alignment

Protein sequence 177 aa MARRLPKPTLQG ... DTAPRGARKKQ\*

Protein sequence 1129 aa MQGAQTSEDNLG ... RLATVLPGLEV\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 15.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:1 (SEQ ID NO:2) with the amino acid sequence, BA-LF2, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

-----
1  MQGAQTSEDNLGSGSQPGPCGYIIFYPLATYPLREVATLGTGYAGHRCLTVPLLCGITVE 60
   .                20                .                40                .                60
-----
61  PGFSINVKALHRRPDPNCGLLRATSYHRDIYVFHNAHMPPIFEGPGLEALCGETREVF 120
   .                80                .                100               .                120
-----
121 YDAYSALPRESSKPGDFFPEGLDPSAYLGAVAITEAFKERLYSGNLVAIPSLKQEVAVGQ 180
   .                140               .                160               .                180
-----
181 SASVRVPLYDKEVFPEGVPQLRQFYNSDLSRCMHEALYTGLAQALRVRVVGKLVLELEKQ 240
   .                200               .                220               .                240
-----
241 SLQDQAKVAKVAPLKEFPASTISHPDGALMIVDSAACELAVSYAPAMLEASHETPASLN 300
   .                260               .                280               .                300
-----
301 YDSWPLFADCEGPEARVAALHRYNASLAPHVSTQIFATNSVLYVSGVSKSTGQGKESLFN 360
   .                320               .                340               .                360
-----
361 SFYMTHTGLGTLQEGTWDPCCRPCFSGWGGPDVTGTNGPGNYAVEHLVYAASFSPNLLARY 420
   .                380               .                400               .                420
-----
421 AYYLQFCQGQKSSLTVPVETGSYVAGAAASPMCSLCEGRAPAVCLNTLFFRLRDRFPPVM 480
   .                440               .                460               .                480
-----
481 STQRRDPYVISGASGSYNETDFLGNFLNFIDKEDDGQRPDDEPRYTYWQLNQNLLERLSR 540
   .                500               .                520               .                540
-----
541 LGIDAEGKLEKEPHGPRDFVKMFKDVAADVAEVEVQFMNSMAKNNITYKDLVKSCYHVMQ 600
   .                560               .                580               .                600

```

601 YSCNPFAQPACPIFTQLFYRSLLTILQDISLPICMCYENDNPGLGQSPPEWLKGHYQTLC 660  
 . 620 . 640 . 660

661 TNFRSLAIDKGVLTAKVAVHGEPTCDLPDLDAALQGRVYGRRLPVRMSKVLMLCPRNI 720  
 . 680 . 700 . 720

721 KIKNRVVFTGENAALQNSFIKSTTRRENYIINGPYMKFLNTYHKTLFPDTKLSSLYLWHN 780  
 . 740 . 760 . 780

781 FSRRRSVPVPSGASAE EYSDLALFVDGG SRAHEESNVIDVVPGNLV TYAKQRLNNA ILKA 840

841 CGQTQFYISLIQGLVPRTQSVPARDYPHVLGTRAVESAAAYAEATSSLTATTVVCAATDC 900

1 -----MARRLPKP 8

901 LSQVCKARPVVTLPTINKYTG VNGNNQIFQAGNLGYFMGRGVDRNLLQAPGAGLRKQAG 960

• 20 • 40 • 60

9 TLQGRLEADFPDSPLLPKFQELNQNNLPNDVFREAQRSYLVFLTSQFCYEEYVORTFGVP 68

961 GSSMRKKFVFATPTLGLTVKRRTPQAATTYEIENIRAGLEAIIISQKQEEDCVFDVVCNLVD 1020

80	100	120
----	-----	-----

69 RRQRAIDKRQRASVAGAGAAHLGGSSATPVQQAQAAASAGTGALASSAPSTAVAQSATP 128

[illegible]

1021 AMGEACASLTRDDAEYLLGRFSVLADSVLETLATIASSGIEWTAEAAARDFLEGVWGGGPGA 1080  
 . 1040 . 1060 . 1080

• 140 • 160 •

129 SVSSSISSLRAATSGATAAASAAA AVDTGSGGGGQPHDTAPRGARKKQ\* 177

XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

```

1081 AQDNFISVAEPVSTASQASAGLLGGGGQGS GGRKRRLATVLPGLV*      1129
      .              1100      .              1120

```

% Identity = 0.0 (0/1129)      % Homology = 0.0 (0/1129)      % Total = 0.0 (0/1129)

```
% Total = 0.0 (0/1129)
```

///

9310-13DVCTDV SEQ ID NO 4.xprt x Bankier et al. BA-LF2.xprt => Protein Alignment

Protein sequence 346 aa MLSGNAGEGATA ... FCEELLNKRVA\*

Protein sequence 1129 aa MQGAQTSEDNLG ... RLATVLPGLEV\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 16.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:3 (SEQ ID NO:4) with the amino acid sequence, BA-LF2, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

-----
1 MQGAQTSEDNLGSQSQPGPCGYIYFYPLATYPLREVATLGTGYAGHRCLTVPLLCGITVE 60
  .                20                .                40                .                60
-----
61 PGFSINVKALHRRPDPNCGLLRATSYHRDIYVFHNAHNVPPPIFEGPGLEALCGETREVFG 120
  .                80                .                100               .                120
-----
121 YDAYSALPRESSKPGDFFPEGLDPSAYLGAVAITEAFKERLYSGNLVAIPSLKQEVAVGQ 180
  .                140               .                160               .                180
-----
181 SASVRVPLYDKEVFPEGVPQLRQFYNSDLSRCMHEALYTGLAQALRVRVVGKLVELLEKQ 240
  .                200               .                220               .                240
-----
241 SLQDQAKVAKVAPLKEFPASTISHPDSGALMIVDSAACELAVSYAPAMLEASHETPASLN 300
  .                260               .                280               .                300
-----
301 YDSWPLFADCEGPEARVAALHRYNASLAPHVSTQIFATNSVLYVSGVSKSTGQGKESLFN 360
  .                320               .                340               .                360
-----
361 SFYMTHGLGTLQEGTWDPCCRPCFSGWGGPDVTGTNGPGNYAVEHLVYAASFSPNLLARY 420
  .                380               .                400               .                420
-----
421 AYYLQFCQGQKSSLTPVPETGSYVAGAAASPMCSLCEGRAPAVCLNTLFFRLRDRFPPVM 480
  .                440               .                460               .                480
-----
481 STQRRDPYVISGASGSYNETDFLGNFLNFIDKEDDGQRPDDEPRYTYWQLNQNLRLSLR 540
  .                500               .                520               .                540
-----
541 LGIDAEGKLEKEPHGPRDFVKMFKDVDAAVDAEVVQFMNSMAKNNITYKDLVKSCYHVMQ 600
  .                560               .                580               .                600

```

```

-----
601 YSCNPFAQPAQPIFTQLFYRSLTILQDISLPICMCYENDNPGLGQSPPEWLKGHYQTL 660
      .               620               .               640               .               660
-----

661 TNFRSLAIDKGVLTAKKVVHGEPTCDLPDLDAALQGRVYGRRLPVRMSKVLMLCPRNI 720
      .               680               .               700               .               720
-----

721 KIKNRVVFTEGENAALQNSFIKSTTRRENIINGPYMKFLNTYHKTLPDTKLSSLYLWHN 780
      .               740               .               760               .               780
      .               20               .               40               .               60
1 ---MLSGNAGEGATACGGSAAAGQDLISVPRNTFMTLLQTNLDNKPPRQTPLPYAAPLPP 57
      .               .               .               .               .               .
      .               .               .               .               .               .
781 FSRRRSVPVPSGASAEYSDLALFVDGGSRAHEESNVIDVPGNLVTYAKQRLNNAILKA 840
      .               800               .               820               .               840
      .               60               .               80               .               100
58 FSHQAIATAPSYGPGAGAVAPAGGYFTSPGGYYAGPAGGDPGAFLAMDAHTYHPHPPPP 117
      .               .               .               .               .               .
      .               .               .               .               .               .
841 CGQTQFYISLIQGLVPRTQSVPARDYPHVLGTRAVESAAAYAEATSSLTATTVVCAATDC 900
      .               860               .               880               .               900
      .               120               .               140               .               160
118 AYFGLPGLFGPPPPCLLTDSHLRADYVPAPSRSNKRKRDPEDDEEGGLFPGEDATLYR 177
      .               .               .               .               .               .
      .               .               .               .               .               .
901 LSQVCKARPVVTLPVTINKYTGVMGNNQIFQAGNLGYFMGRGVDRNLLQAPGAGLRKQAG 960
      .               920               .               940               .               960
      .               180               .               200               .               220
178 KDIAGLSKSVNELQHTLQALRRETLSYGHTGVGYCPQQGPCYTHSGPYGFQPHQSYEVPR 237
      .               .               .               .               .               .
      .               .               .               .               .               .
961 GSSMRKKFVFATPTLGLTVKRRTQAATTYEIENIRAGLEAIIISQKQEDCVFDVVCNLDV 1020
      .               980               .               1000               .               1020
      .               240               .               260               .               280
238 YVPHPPPPPTSHQAAQAQPPPPGTQAPEAHCVAESTIPEAGAAGNSGPREDTNPQQPTTE 297
      .               .               .               .               .               .
      .               .               .               .               .               .
1021 AMGEACASLTRDDAEYLLGRFSVLADSVLETLATIASSGIEWTAEAAARDFLEGVWGGPGA 1080
      .               1040               .               1060               .               1080
      .               300               .               320               .               340
298 GHHRGKKLVQASASGVAQSKEPTTPKAKSVSAHLKSIFCEELLNKRVA* 346
      .               .               .               .               .               .
      .               .               .               .               .               .
1081 AQDNFISVAEPVSTASQASAGLLGGGGQSGGRRKRRLATVLPGLEV* 1129
      .               1100               .               1120

```

% Identity = 0.0 (0/1129)      % Homology = 0.0 (0/1129)      % Total = 0.0 (0/1129)

///



9310-13DVCTDV SEQ ID NO 5.xprt x Bankier et al. BA-LF2.xprt => Protein Alignment

Protein sequence 24 aa AVDTGSGGGGQP ... HDTAPRGARKKQ

Protein sequence 1129 aa MQGAQTSIEDNLG ... RLATVLPGLLEV\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

Alignment 17. Comparison of the amino acid sequence of SEQ ID NO:5 with the amino acid sequence, BA-LF2, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

-----
1 MQGAQTSIEDNLGSQSQPGPCGYIYFYPLATYPLREVATLGTGYAGHRCLTVPLLCGITVE 60
  .                20                .                40                .                60
-----
61 PGFSINVKALHRRPDPNCGLLRATSYHRDIYVFHNAHMPPIFEGPGLEALCGETREVFG 120
  .                80                .                100               .                120
-----
121 YDAYSALPRESSKPGDFFPEGLDPSAYLGAVAITEAFKERLYSGNLVAIPSLKQEVAVGQ 180
  .                140               .                160               .                180
-----
181 SASVRVPLYDKEVFPEGVPQLRQFYNSDLSCMHEALYTGLAQALRVRVVGKLVLELEKQ 240
  .                200               .                220               .                240
-----
241 SLQDQAKVAKVAPLKEFPASTISHPDGALMIVDSAACELAVSYAPAMLEASHETPASLN 300
  .                260               .                280               .                300
-----
301 YDSWPLFADCEGPEARVAALHRYNASLAPHVSTQIFATNSVLYVSGVSKSTGQGKESLFN 360
  .                320               .                340               .                360
-----
361 SFYMTHTGLGTLQEGTWDPGRRPCFSGWGGPDVTGTNGPGNYAVEHLVYAASFSPNLLARY 420
  .                380               .                400               .                420
-----
421 AYYLQFCQGQKSSLTPVPETGSYVAGAAASPMCSLCEGRAPAVCLNTLFFRLRDRFPPVM 480
  .                440               .                460               .                480
-----
481 STQRRDPYVISGASGSYNETDFLGNFLNFIDKEDDQRPDDEPRYTYWQLNQNLRLSR 540
  .                500               .                520               .                540
-----
541 LGIDAEGKLEKEPHGPRDFVKMFKDVDAAVDAEVVQFMNSMAKNNITYKDLVKSCYHVMQ 600
  .                560               .                580               .                600

```

```

-----
601 YSCNPFAQPACPIFTQLFYRSLTILQDISLPICMCYENDNPGLGQSPPEWLKGHYQTLC 660
      .           620           .           640           .           660
-----
661 TNFRSLAIDKGVLTAKEAKVVHGEPTCDLPDLDAALQGRVYGRRLPVRMSKVLMLCPRNI 720
      .           680           .           700           .           720
-----
721 KIKNRVVFTGENAALQNSFIKSTTRRENYIINGPYMKFLNTYHKTLFPDTKLSSLYLWHN 780
      .           740           .           760           .           780
-----
781 FSRRRSVPVPSGASAEYSDLALFVDGGSRAHEESNVIDVVPGNLVITYAKQRLNNAILKA 840
      .           800           .           820           .           840
-----
841 CGQTQFYISLIQGLVPRTQSVPARDYPHVLGTRAVESAAAYAEATSSLTATTVVCAATDC 900
      .           860           .           880           .           900
-----
901 LSQVCKARPVVTLPVTINKYTG VNGNNQIFQAGNLGYFMGRGVDRNLLQAPGAGLRKQAG 960
      .           920           .           940           .           960
-----
961 GSSMRKKFVFATPTLGLTVKRRTQAATTYEIENIRAGLEAIISQKQEEDCVFDVVCNLVD 1020
      .           980           .           1000           .           1020
-----
1021 AMGEACASLTRDDAEYLLGRFSVLADSVLETLATIASSGIEWTAEAAARDFLEGVWGGPGA 1080
      .           1040           .           1060           .           1080
      .           1080           .           1100           .           1120
      .           1120           .           1140           .           1160
      .           1160           .           1180           .           1200
      .           1200           .           1220           .           1240
      .           1240           .           1260           .           1280
      .           1280           .           1300           .           1320
      .           1320           .           1340           .           1360
      .           1360           .           1380           .           1400
      .           1400           .           1420           .           1440
      .           1440           .           1460           .           1480
      .           1480           .           1500           .           1520
      .           1520           .           1540           .           1560
      .           1560           .           1580           .           1600
      .           1600           .           1620           .           1640
      .           1640           .           1660           .           1680
      .           1680           .           1700           .           1720
      .           1720           .           1740           .           1760
      .           1760           .           1780           .           1800
      .           1800           .           1820           .           1840
      .           1840           .           1860           .           1880
      .           1880           .           1900           .           1920
      .           1920           .           1940           .           1960
      .           1960           .           1980           .           2000
      .           2000           .           2020           .           2040
      .           2040           .           2060           .           2080
      .           2080           .           2100           .           2120
      .           2120           .           2140           .           2160
      .           2160           .           2180           .           2200
      .           2200           .           2220           .           2240
      .           2240           .           2260           .           2280
      .           2280           .           2300           .           2320
      .           2320           .           2340           .           2360
      .           2360           .           2380           .           2400
      .           2400           .           2420           .           2440
      .           2440           .           2460           .           2480
      .           2480           .           2500           .           2520
      .           2520           .           2540           .           2560
      .           2560           .           2580           .           2600
      .           2600           .           2620           .           2640
      .           2640           .           2660           .           2680
      .           2680           .           2700           .           2720
      .           2720           .           2740           .           2760
      .           2760           .           2780           .           2800
      .           2800           .           2820           .           2840
      .           2840           .           2860           .           2880
      .           2880           .           2900           .           2920
      .           2920           .           2940           .           2960
      .           2960           .           2980           .           3000
      .           3000           .           3020           .           3040
      .           3040           .           3060           .           3080
      .           3080           .           3100           .           3120
      .           3120           .           3140           .           3160
      .           3160           .           3180           .           3200
      .           3200           .           3220           .           3240
      .           3240           .           3260           .           3280
      .           3280           .           3300           .           3320
      .           3320           .           3340           .           3360
      .           3360           .           3380           .           3400
      .           3400           .           3420           .           3440
      .           3440           .           3460           .           3480
      .           3480           .           3500           .           3520
      .           3520           .           3540           .           3560
      .           3560           .           3580           .           3600
      .           3600           .           3620           .           3640
      .           3640           .           3660           .           3680
      .           3680           .           3700           .           3720
      .           3720           .           3740           .           3760
      .           3760           .           3780           .           3800
      .           3800           .           3820           .           3840
      .           3840           .           3860           .           3880
      .           3880           .           3900           .           3920
      .           3920           .           3940           .           3960
      .           3960           .           3980           .           4000
      .           4000           .           4020           .           4040
      .           4040           .           4060           .           4080
      .           4080           .           4100           .           4120
      .           4120           .           4140           .           4160
      .           4160           .           4180           .           4200
      .           4200           .           4220           .           4240
      .           4240           .           4260           .           4280
      .           4280           .           4300           .           4320
      .           4320           .           4340           .           4360
      .           4360           .           4380           .           4400
      .           4400           .           4420           .           4440
      .           4440           .           4460           .           4480
      .           4480           .           4500           .           4520
      .           4520           .           4540           .           4560
      .           4560           .           4580           .           4600
      .           4600           .           4620           .           4640
      .           4640           .           4660           .           4680
      .           4680           .           4700           .           4720
      .           4720           .           4740           .           4760
      .           4760           .           4780           .           4800
      .           4800           .           4820           .           4840
      .           4840           .           4860           .           4880
      .           4880           .           4900           .           4920
      .           4920           .           4940           .           4960
      .           4960           .           4980           .           5000
      .           5000           .           5020           .           5040
      .           5040           .           5060           .           5080
      .           5080           .           5100           .           5120
      .           5120           .           5140           .           5160
      .           5160           .           5180           .           5200
      .           5200           .           5220           .           5240
      .           5240           .           5260           .           5280
      .           5280           .           5300           .           5320
      .           5320           .           5340           .           5360
      .           5360           .           5380           .           5400
      .           5400           .           5420           .           5440
      .           5440           .           5460           .           5480
      .           5480           .           5500           .           5520
      .           5520           .           5540           .           5560
      .           5560           .           5580           .           5600
      .           5600           .           5620           .           5640
      .           5640           .           5660           .           5680
      .           5680           .           5700           .           5720
      .           5720           .           5740           .           5760
      .           5760           .           5780           .           5800
      .           5800           .           5820           .           5840
      .           5840           .           5860           .           5880
      .           5880           .           5900           .           5920
      .           5920           .           5940           .           5960
      .           5960           .           5980           .           6000
      .           6000           .           6020           .           6040
      .           6040           .           6060           .           6080
      .           6080           .           6100           .           6120
      .           6120           .           6140           .           6160
      .           6160           .           6180           .           6200
      .           6200           .           6220           .           6240
      .           6240           .           6260           .           6280
      .           6280           .           6300           .           6320
      .           6320           .           6340           .           6360
      .           6360           .           6380           .           6400
      .           6400           .           6420           .           6440
      .           6440           .           6460           .           6480
      .           6480           .           6500           .           6520
      .           6520           .           6540           .           6560
      .           6560           .           6580           .           6600
      .           6600           .           6620           .           6640
      .           6640           .           6660           .           6680
      .           6680           .           6700           .           6720
      .           6720           .           6740           .           6760
      .           6760           .           6780           .           6800
      .           6800           .           6820           .           6840
      .           6840           .           6860           .           6880
      .           6880           .           6900           .           6920
      .           6920           .           6940           .           6960
      .           6960           .           6980           .           7000
      .           7000           .           7020           .           7040
      .           7040           .           7060           .           7080
      .           7080           .           7100           .           7120
      .           7120           .           7140           .           7160
      .           7160           .           7180           .           7200
      .           7200           .           7220           .           7240
      .           7240           .           7260           .           7280
      .           7280           .           7300           .           7320
      .           7320           .           7340           .           7360
      .           7360           .           7380           .           7400
      .           7400           .           7420           .           7440
      .           7440           .           7460           .           7480
      .           7480           .           7500           .           7520
      .           7520           .           7540           .           7560
      .           7560           .           7580           .           7600
      .           7600           .           7620           .           7640
      .           7640           .           7660           .           7680
      .           7680           .           7700           .           7720
      .           7720           .           7740           .           7760
      .           7760           .           7780           .           7800
      .           7800           .           7820           .           7840
      .           7840           .           7860           .           7880
      .           7880           .           7900           .           7920
      .           7920           .           7940           .           7960
      .           7960           .           7980           .           8000
      .           8000           .           8020           .           8040
      .           8040           .           8060           .           8080
      .           8080           .           8100           .           8120
      .           8120           .           8140           .           8160
      .           8160           .           8180           .           8200
      .           8200           .           8220           .           8240
      .           8240           .           8260           .           8280
      .           8280           .           8300           .           8320
      .           8320           .           8340           .           8360
      .           8360           .           8380           .           8400
      .           8400           .           8420           .           8440
      .           8440           .           8460           .           8480
      .           8480           .           8500           .           8520
      .           8520           .           8540           .           8560
      .           8560           .           8580           .           8600
      .           8600           .           8620           .           8640
      .           8640           .           8660           .           8680
      .           8680           .           8700           .           8720
      .           8720           .           8740           .           8760
      .           8760           .           8780           .           8800
      .           8800           .           8820           .           8840
      .           8840           .           8860           .           8880
      .           8880           .           8900           .           8920
      .           8920           .           8940           .           8960
      .           8960           .           8980           .           9000
      .           9000           .           9020           .           9040
      .           9040           .           9060           .           9080
      .           9080           .           9100           .           9120
      .           9120           .           9140           .           9160
      .           9160           .           9180           .           9200
      .           9200           .           9220           .           9240
      .           9240           .           9260           .           9280
      .           9280           .           9300           .           9320
      .           9320           .           9340           .           9360
      .           9360           .           9380           .           9400
      .           9400           .           9420           .           9440
      .           9440           .           9460           .           9480
      .           9480           .           9500           .           9520
      .           9520           .           9540           .           9560
      .           9560           .           9580           .           9600
      .           9600           .           9620           .           9640
      .           9640           .           9660           .           9680
      .           9680           .           9700           .           9720
      .           9720           .           9740           .           9760
      .           9760           .           9780           .           9800
      .           9800           .           9820           .           9840
      .           9840           .           9860           .           9880
      .           9880           .           9900           .           9920
      .           9920           .           9940           .           9960
      .           9960           .           9980           .           10000
      .           10000          .           10020          .           10040
      .           10040          .           10060          .           10080
      .           10080          .           10100          .           10120
      .           10120          .           10140          .           10160
      .           10160          .           10180          .           10200
      .           10200          .           10220          .           10240
      .           10240          .           10260          .           10280
      .           10280          .           10300          .           10320
      .           10320          .           10340          .           10360
      .           10360          .           10380          .           10400
      .           10400          .           10420          .           10440
      .           10440          .           10460          .           10480
      .           10480          .           10500          .           10520
      .           10520          .           10540          .           10560
      .           10560          .           10580          .           10600
      .           10600          .           10620          .           10640
      .           10640          .           10660          .           10680
      .           10680          .           10700          .           10720
      .           10720          .           10740          .           10760
      .           10760          .           10780          .           10800
      .           10800          .           10820          .           10840
      .           10840          .           10860          .           10880
      .           10880          .           10900          .           10920
      .           10920          .           10940          .           10960
      .           10960          .           10980          .           11000
      .           11000          .           11020          .           11040
      .           11040          .           11060          .           11080
      .           11080          .           11100          .           11120
      .           11120          .           11140          .           11160
      .           11160          .           11180          .           11200
      .           11200          .           11220          .           11240
      .           11240          .           11260          .           11280
      .           11280          .           11300          .           11320
      .           11320          .           11340          .           11360
      .           11360          .           11380          .           11400
      .           11400          .           11420          .           11440
      .           11440          .           11460          .           11480
      .           11480          .           11500          .           11520
      .           11520          .           11540          .           11560
      .           11560          .           11580          .           11600
      .           11600          .           11620          .           11640
      .           11640          .           11660          .           11680
      .           11680          .           11700          .           11720
      .           11720          .           11740          .           11760
      .           11760          .           11780          .           11800
      .           11800          .           11820          .           11840
      .           11840          .           11860          .           11880
      .           11880          .           11900          .           11920
      .           11920          .           11940          .           11960
      .           11960          .           11980          .           12000
      .           12000          .           12020          .           12040
      .           12040          .           12060          .           12080
      .           12080          .           12100          .           12120
      .           12120          .           12140          .           12160
      .           12160          .           12180          .           12200
      .           12200          .           12220          .           12240
      .           12240          .           12260          .           12280
      .           12280          .           12300          .           12320
      .           12320          .           12340          .           12360
      .           12360          .           12380          .           12400
      .           12400          .           12420          .           12440
      .           12440          .           12460          .           12480
      .           12480          .           12500          .           12520
      .           12520          .           12540          .           12560
      .           12560          .           12580          .           12600
      .           12600          .           12620          .           12640
      .           12640          .           12660          .           12680
      .           12680          .           12700          .           12720
      .           12720          .           12740          .           12760
      .           12760          .           12780          .           12800
      .           12800          .           12820          .           12840
      .           12840          .           12860          .           12880
      .           12880          .           12900          .           12920
      .           12920          .           12940          .           12960
      .           12960          .           12980          .           13000
      .           13000          .           13020          .           13040
      .           13040          .           13060          .           13080
      .           13080          .           13100          .           13120
      .           13120          .           13140          .           13160
      .           13160          .           13180          .           13200
      .           13200          .           13220          .           13240
      .           13240          .           13260          .           13280
      .           13280          .           13300          .           13320
      .           13320          .           13340          .           13360
      .           13360          .           13380          .           13400
      .           13400          .           13420          .           13440
      .           13440          .           13460          .           13480
      .           13480          .           13500          .           13520
      .           13520          .           13540          .           13560
      .           13560          .           13580          .           13600
      .           13600          .           13620          .           13640
      .           13640          .           13660          .           13680
      .           13680          .           13700          .           13720
      .           13720          .           13740          .           13760
      .           13760          .           13780          .           13800
      .           13800          .           13820          .           13840
      .           13840          .           13860          .           13880
      .           13880          .           13900          .           13920
      .           13920          .           13940          .           13960
      .           13960          .           13980          .           14000
      .           14000          .           14020          .           14040
      .           14040          .           14060          .           14080
      .           14080          .           14100          .           14120
      .           14120          .           14140          .           14160
      .           14160          .           14180          .           14200
      .           14200          .           14220          .           14240
      .           14240          .           14260          .           14280
      .           14280          .           14300          .           14320
      .           14320          .           14340          .           14360
      .           14360          .           14380          .           14400
      .           14400          .           14420          .           14440
      .           14440          .           14460          .           14480
      .           14480          .           14500          .           14520
      .           14520          .           14540          .           14560
      .           14560          .           14580          .           14600
      .           14600          .           14620          .           14640
      .           14640          .           14660          .           14680
      .           14680          .           14700          .           14720
      .           14720          .           14740          .           14760
      .           14760          .           14780          .           14800
      .           14800          .           14820          .           14840
      .           14840          .           14860          .           14880
      .           14880          .           14900          .           14920
      .           14920          .           14940          .           14960
      .           14960          .           14980          .           15000
      .           15000          .           15020          .           15040
      .           15040          .           15060          .           15080
      .           15080          .           15100          .           15120
      .           15120          .           15140          .           15160
      .           15160          .           15180          .           15200
      .           15200          .           15220          .           15240
      .           15240          .           15260          .           15280
      .           15280          .           15300          .           15320
      .           15320          .           15340          .           15360
      .           15360          .           15380          .           15400
      .           15400          .           15420          .           15440
      .           15440          .           15460          .           15480
      .           15480          .           15500          .           15520
      .           15520          .           15540          .           15560
      .           15560          .           15580          .           15600
      .           15600          .           15620          .           15640
      .           15640          .           15660          .           15680
      .           15680          .           15700          .           15720
      .           15720          .           15740          .           15760
      .           15760          .           15780          .           15800
      .           15800          .           15820          .           15840
      .           15840          .           15860          .           15880
      .           15880          .           15900          .           15920
      .           15920          .           15940          .           15960
      .           15960          .           15980          .           16000
      .           16000          .           16020          .           16040
      .           16040          .           16060          .           16080
      .           16080          .           16100          .           16120
      .           16120          .           16140          .           16160
      .           16160          .           16180          .           16200
      .           16200          .           16220          .           16240
      .           16240          .           16260          .           16280
      .           16280          .           16300          .           16320
      .           16320          .           16340          .           16360
      .           16360          .           16380          .           16400
      .           16400          .           16420          .           16440
      .           16440          .           16460          .           16480
      .           16480          .           16500          .           16520
      .           16520          .           16540          .           16560
      .           16560          .           16580          .           16600
      .           16600          .           16620          .           16640
      .           16640          .           16660          .           16680
      .           16680          .           16700          .           16720
      .           16720          .           16740          .           16760
      .           16760          .           16780          .           16800
      .           16800          .           16820          .           16840
      .           16840          .           16860          .           16880
      .           16880          .           16900          .           16920
      .           16920          .           16940          .           16960
      .           16960          .           16980          .           17000
      .           17000          .           17020          .           17040
      .           17040          .           17060          .           17080
      .           17080          .           17100          .           17120
      .           17120          .           17140          .           17160
      .           17160          .           17180          .           17200
      .           17200          .           17220          .           17240
      .           17240          .           17260          .           17280
      .           17280          .           17300          .           17320
      .           17320          .           17340          .           17360
      .           17360          .           17380          .           17400
      .           17400          .           17420          .           17440
      .           17440          .           17460          .           17480
      .           17480          .           17500          .           17520
      .           17520          .           17540          .           17560
      .           17560          .           17580          .           17600
      .           17600          .           17620          .           17640
      .           17640          .           17660          .           17680
      .           17680          .           17700          .           17720
      .           17720          .           17740          .           17760
      .           17760          .           17780          .           17800
      .           17800          .           17820          .           17840
      .           17840          .           17860          .           17880
      .           17880          .           17900          .           17920
      .           17920          .           17940          .           17960
      .           17960          .           17980          .           18000
      .           18000          .           18020          .           18040
      .           18040          .           18060          .           18080
      .           18080          .           18100          .           18120
      .           18120          .           18140          .           18160
      .           18160          .           18180          .           18200
      .           18200          .           18220          .           18240
      .           18240          .           18260          .           18280
      .           18280          .           18300          .           18320
      .           18320          .           18340          .           18360
      .           18360          .           18380          .           18400
      .           18400          .           18420          .           18440
      .           18440          .           18460          .           18480
      .           18480          .           18500          .           18520
      .           18520          .           18540          .           18560
      .           18560          .           18580          .           18600
      .           18600          .           18620          .           18640
      .           18640          .           18660          .           18680
      .           18680          .           18700          .           18720
      .           18720          .           18740          .           18760
      .           18760          .           18780          .           18800
      .           18800          .           18
```

9310-13DVCTDV SEQ ID NO 6.xprt x Bankier et al. BA-LF2.xprt => Protein Alignment

Protein sequence 30 aa STAVAQSATPSV ... LRAATSGATAAA

Protein sequence 1129 aa MQGAQTSEDNLG ... RLATVLPGLEV\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 18.** Comparison of the amino acid sequence of SEQ ID NO:6 with the amino acid sequence, BA-LF2, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

-----
1 MQGAQTSEDNLG SQSQPGPCGYIYFYPLATYPLREVATLGTGYAGHRCLTVPLLCGITVE 60
   .                20                .                40                .                60
-----
61 PGFSINVKALHRRPDPNCGLLRATSYHRDIYVFHNAHMPPIFEGPGLEALCGETREVFG 120
   .                80                .                100               .                120
-----
121 YDAYSALPRESSKPGDFFPEGLDPSAYLGAVAITEAFKERLYSGNLVAIPSLKQEVAVGQ 180
   .                140               .                160               .                180
-----
181 SASVRVPLYDKEVFPFEGVPQLRQFYNSDLSRCMHEALYTGLAQALRVRRVGKLVELLEKQ 240
   .                200               .                220               .                240
-----
241 SLQDQAKVAKVAPLKEFPASTISHPD SGALMIVDSAACELAVSYAPAMLEASHETPASLN 300
   .                260               .                280               .                300
-----
301 YDSWPLFADCEGPEARVAALHRYNASLAPHVSTQIFATNSVLYVSGVSKSTGQGKESLFN 360
   .                320               .                340               .                360
-----
361 SFYMT HGLGTLQEGTWDPCRRPCFSGWGGPDVTGTNGPGNYAVEHLVYAASFSPNLLARY 420
   .                380               .                400               .                420
-----
421 AYYLQFCQGQKSSLTPVPETGSYVAGAAASPMCSLCEGRAPAVCLNTLFFRLRDRFPVPM 480
   .                440               .                460               .                480
-----
481 STQRRDPYVISGASGSYNETDFLGNFLNFIDKEDDGQRPDDEPRYTYWQLNQNLLERLSR 540
   .                500               .                520               .                540
-----
541 LGIDAEGKLEKEPHGPRDFVKMFKDVDAAVDAEVVQFMNSMAKNNITYKDLVKSCYHVMQ 600
   .                560               .                580               .                600

```

```

-----
601 YSCNPFAQPACPIFTQLFYRSLLTILQDISLPICMCYENDNPGLGQSPPEWLKGHYQTL 660
      .               620               .               640               .               660
-----
661 TNFRSLAIDKGVLTAKAKVVHGEPTCDLPDLDAALQGRVYGRRLPVRMSKVLMLCPRNI 720
      .               680               .               700               .               720
-----
721 KIKNRVVFTGENAALQNSFIKSTTRRENYIINGPYMKFLNTYHKTLFPDTKLSSLYLWHN 780
      .               740               .               760               .               780
-----
781 FSRRRSVPVPSGASAEYSDLALFVDGGSRAHEESNVIDVVPGNLVTYAKQRLNNAILKA 840
      .               800               .               820               .               840
-----
841 CGQTQFYISLIQGLVPRTQSVPARDYPHVLGTRAVESAAAYAEATSSLTATTVVCAATDC 900
      .               860               .               880               .               900
-----
901 LSQVCKARPVVTLPTVTINKYTG VNGNNQIFQAGNLGYFMGRGVDRNLLQAPGAGLRKQAG 960
      .               920               .               940               .               960
-----
961 GSSMRKKFVFATPTLGLTVKRRTQAATTYEIENIRAGLEAIISQKQEDCVFDVVCNLVD 1020
      .               980               .               1000               .               1020
-----
1021 AMGEACASLTRDDAEYLLGRFSVLADSVLETLATIASSGIEWTAEAAARDFLEGVWGGPGA 1080
      .               1040               .               1060               .               1080
      .               20
1  -----STAVAQSATPSVSSSISSLRAATSGATAAA 30
      .               .               .               .               .               .
      .               .               .               .               .               .
      .               .               .               .               .               .
1081 AQDNFISVAEPVSTASQASAGLLGGGGQSGGRRKRRLATVLPGLEV* 1129
      .               1100               .               1120
-----
% Identity = 0.0 (0/1129)      % Homology = 0.0 (0/1129)      % Total = 0.0 (0/1129)

```

///

9310-13DVCTDV SEQ ID NO 2.xprt x Bankier et al. BA-LF1.xprt => Protein Alignment

Protein sequence 177 aa MARRLPKPTLQG ... DTAPRGARKKQ\*

Protein sequence 221 aa MNLAIALDSPHP ... LASLTDFLKSL\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 19.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:1 (SEQ ID NO:2) with the amino acid sequence, BA-LF1, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .           20           .           40           .           60
1  MARRLPKPTLQGRLEADFPDSPLLPKFQELNQNNLPNDVFREAQRSYLVFLTSQFCYEEY 60
   M  +  +  L A  +  P           L  + P++ R A+ +  VF+ +  E  +
1  MNLAIALDSPHPGL=ASYTILPRPFYHISLKPVSWPDETMRPAKSTDSVFVRTPV==EAW 57
      .           20           .           40           .
      .           80           .           100          .
61  VQRTFGVPRRQRAIDKRQRASVAGAGAHHLGGSSATPVQQAQAAASAGTGAL-ASSAPS 119
   V  +  +  +  RA  A           A  +  +  A+           L A  A
58  VAPSPDDKVAESSYLMFRAMYAVFTRDEKDLPLPALVLCRLIKASLRKDRKLYAELACR 117
   60           .           80           .           100          .
   120          .           140          .           160          .
120  TAVAQSATPSVSSSISSLRAATSGATAAASAAAAMD--TGSGGGGQPHDTAPRGARKKQ* 177
   TA           V  IS LRA  +  S           V  T           D           A
118  TADIGGKDTHVRLIISVLRVYNDHYDYSRLRVVLCYTVVFAVRNYLDDHKSAAFVLGA 177
   120          .           140          .           160          .

-----

178  IAHYLALYRRLWFARLGGMPRLRRQFPVTWALASLTDFLKSL*                221
   180          .           200          .           220

```

% Identity = 14.7 (33/224)      % Homology = 8.0 (18/224)      % Total = 22.8 (51/224)

///

9310-13DVCTDV SEQ ID NO 4.xprt x Bankier et al. BA-LF1.xprt => Protein Alignment

Protein sequence 346 aa MLSGNAGEGATA ... FCEELLNKRVA\*

Protein sequence 221 aa MNLAIALDSPHP ... LASLTDFLKSL\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 20.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:3 (SEQ ID NO:4) with the amino acid sequence, BA-LF1, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .           20           .           40           .           60
1  M L S G N A G E G A T A C G S A A A G Q D L I S V P R N T F M T L L Q T N L D N K P P R Q T P L P Y A A P L P P F S H 60
   M   A +       G   A +       +   +   +   + P + T   +   P   +
1  M N L A I A L D S P H P = G L = A S Y T I L P R P F Y H I S L K P V S W P D E T M R P A K S T D S V F V R T = P V E A W 57
      .           20           .           40           .           60
61 Q A I A T A P S Y G P G A G A V A P A G G Y F T S P G G Y Y A G P A G G D P G A F L A M D A H T Y H P H P P P P A Y F 120
   A +       +   +   Y       P       L   +       +   A
58 V A P S P P D D K V A E S S Y L M F R A M Y A V F T R D E K D L P L P A L V L C R L I K A S L R K D R K L Y A E L A C R 117
   60           .           80           .           100           .           120
121 G L P G L F G P P P C L L T T D S H L R A D Y V P A P S R S N K R K R D P E E D E E G G L F P G E D A T L Y R K D I 180
     G       L   S L R A Y       + R R       +   D       +
118 T A D I G = G K D T H V R L I I = S V L R A V Y N D H Y D Y W S = R L R V V L C Y T V V F A V R N Y L D D H K S A A F V 174
   120           .           140           .           160           .           180
181 A G L S K S V N E L Q H T L Q A L R R E T L S Y G H T G V G Y C P Q Q G P C Y T H S G P Y G F Q P H Q S Y E V P R Y V P 240
     G       L   L   R   +       T
175 L G A I A H Y L A L Y R R L W F A R L G G M P R S L R R Q F P V T W A L A S L T D F L K S L * = = = = = = = = = = = = 221
   180           .           200           .           220           .           240
241 H P P P P P T S H Q A A Q A Q P P P P G T Q A P E A H C V A E S T I P E A G A A G N S G P R E D T N P Q Q P T T E G H H 300
      .           260           .           280           .           300
=====
      .           320           .           340
301 R G K K L V Q A S A S G V A Q S K E P T T P K A K S V S A H L K S I F C E E L L N K R V A * 346
=====

```

% Identity = 7.8 (27/346)      % Homology = 5.2 (18/346)      % Total = 13.0 (45/346)

///

9310-13DVCTDV SEQ ID NO 5.xprt x Bankier et al. BA-LF1.xprt => Protein Alignment

Protein sequence 24 aa AVDTGSGGGGQP ... HDTAPRGARKKQ

Protein sequence 221 aa MNLAIALDSPHP ... LASLTDFLKSL\*

Method: Diagonals (BLOSUM62)  
 Layout: Standard  
 Block Length ≤: 6-aa  
 Mismatch penalty: Smaller (1)  
 Gap penalty: Medium (2)  
 Display: BLOSUM62

Alignment 21. Comparison of the amino acid sequence of  
 SEQ ID NO:5 with the amino acid sequence, BA-LF1, encoded  
 by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .
      20
1 ---AVDTGSGGGGQPHDTA-PRGARKKQ----- 24
      A+  S  G  T  PR
1 MNLAIALDSPHPGLASYTILPRPFYHISLKPVSWPDETMRPAKSTDSVFVRTPVEAWVAP 60
      .
      20
      .
      40
      .
      60

-----

61 SPPDDKVAESSYLMFRAMYAVFTRDEKDLPLPALVLCRLIKASLRKDRKLYAELACRTAD 120
      .
      80
      .
      100
      .
      120

-----

121 IGGKDTHVRLIISVLRAVYNDHYDYSRLRVVLCYTVVFAVRNYLDDHKSAAFVLGAIAH 180
      .
      140
      .
      160
      .
      180

-----

181 YLALYRRLWFARLGGMPRSLRRQFPVTWALASLTDFLKSL* 221
      .
      200
      .
      220
    
```

% Identity = 2.7 (6/221) % Homology = 0.5 (1/221) % Total = 3.2 (7/221)

///

9310-13DVCTDV SEQ ID NO 6.xprt x Bankier et al. BA-LF1.xprt => Protein Alignment

Protein sequence 30 aa STAVAQSATPSV ... LRAATSGATAAA

Protein sequence 221 aa MNLAIALDSPHP ... LASLTDFLKSL\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

Alignment 22. Comparison of the amino acid sequence of SEQ ID NO:6 with the amino acid sequence, BA-LF1, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .               20               .
1 ST-AVAQ-SATPSVSSSISSLRAATSGATAAA----- 30
   A+A S P ++S R +
1 MNLAIALDSPHPGLASYTILPRPFYHISLKPVSWPDETMRPASTDSVFVRTPVEAWVAP 60
   .               20               .               40               .               60
-----
61 SPPDDKVAESSYLMFRAMYAVFTRDEKDLPLPALVLCRLIKASLRKDRKLYAELACRTAD 120
   .               80               .               100               .               120
-----
121 IGGKDTHVRLIISVLRAVYNDHYDYSRLRVVLCYTVVFAVRNYLDDHKSAAFVLGAIAH 180
   .               140               .               160               .               180
-----
181 YLALYRRLW FARLGGMP RSLRRQFPVTWALASLTDFLKSL* 221
   .               200               .               220

```

% Identity = 2.7 (6/221) % Homology = 1.8 (4/221) % Total = 4.5 (10/221)

///



9310-13DVCTDV SEQ ID NO 2.xprt x Bankier et al. BA-RF1.xprt => Protein Alignment

Protein sequence 177 aa MARRLPKPTLQG ... DTAPRGARKKQ\*

Protein sequence 222 aa MARFIAQLLLLL ... HGVYVSGYLSQ\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 23.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:1 (SEQ ID NO:2) with the amino acid sequence, Ba-RF1, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .           20           .           40           .
1  MARRLPKPTLQGRLEADFPDSPL-LPKFQELNQNNLPNDVFREAQRSYLVFLTSQFCYEE 59
   MAR + + L      A      L + L      + E + S+      +
1  MARFIAQLLLLLASCVAAGQAVTAFLGERVTLTSYWRRVSLGPEIEVSWFKLGPGEEQVLI 60
      .           20           .           40           .           60
60  YVQRTFGVPRRQRAIDKRQRASVAGAGAHHLGGSSATPVQQAQAAASAGTGALASSAPS 119
      +           A           + +           T           S
61  GRMHHDVIFIEWPFRGFFDIHRSANTFFLVVTAANISHDGNILCRMKLGETEVTKQEHLS 120
      .           80           .           100          .           120
120 TAVAQSATP-SVSSSISSLRAATSGATAAASAAAAVDTGSGGGGQPHDTAPRGARKKQ*- 177
      + + S S      T T A      V      G +P TA G      K+
121 VVKPLTLSVHSERSQFPDFSVLTVTCTVNAFPHPHVQWLMPEGVEPAPTAANGGVMKEKD 180
      .           140          .           160          .           180

```

```

-----
181 GSLSVAVDLSLPKPWHLPVTCVKGNDKEEAHGVYVSGYLSQ*                222
      .           200          .           220

```

% Identity = 10.8 (24/222)      % Homology = 6.3 (14/222)      % Total = 17.1 (38/222)

///

9310-13DVCTDV SEQ ID NO 4.xprt x Bankier et al. BA-RF1.xprt => Protein Alignment

Protein sequence 346 aa MLSGNAGEGATA ... FCEELLNKRVA\*

Protein sequence 222 aa MARFIAQLLLLA ... HGVIYVSGYLSQ\*

Method: Diagonals (BLOSUM62) Alignment 24. Comparison of the amino acid sequence  
 Layout: Standard encoded by the nucleotide sequence of SEQ ID NO:3  
 Block Length ≤: 6-aa (SEQ ID NO:4) with the amino acid sequence, Ba-RF1,  
 Mismatch penalty: Smaller (1) encoded by the nucleotide sequence of Fig. 2 of Bankier et al.  
 Gap penalty: Medium (2)  
 Display: BLOSUM62

```

      .           20           .           40           .           60
1 MLSGNAGEGATACGGSAAAGQDLISVPRNTFMTLLQTNLDNKPPRQTPLPYAAPLPPFSH 60
=====
      .           80           .           100          .           120
61 QAIATAPSYGPGAGAVAPAGGYFTSPGGYYAGPAGGDPGAFLAMDAHTYHPHPHPPPAYF 120
      .                                     A F
1 =====MARF 4
      .           140          .           160          .           180
121 GLPGLFGPPPPCLLTDSHLRADYVPAPSRSNKRKRDPEDDEEGGLFPGEDATLYRKDI 180
      L           +       + V   S   +       PE +       L PGE+   L   +
.5 IAQLLLLASCVAAGQAVTAFLGERVTLTSYWRRVSLGPEIEVSWFKLGPGEEQVLIGRMH 64
      .           20           .           40           .           60
181 AGLSKSVNELQHTLQALRRRETLSYGHTGVGYCPQQGPCYTHSGPYGFQPHQSYEVPRYVP 240
      +       +       R       +       G   Y       G       E       V
65 HDVIFIEWPFRGFFDIHRSANTFFLVVTAANISHDG=NYLCRMKLGETEVTKQE=HLSV= 121
      .           80           .           100          .           120
241 HPPPPPTSHQAAQAQPPPPGTQAPEAHCVAESTIPEAGAAGNSGPREDTNPQQPTTEGHH 300
      P   S   +   ++Q   P   +       V       P       G   E   P       G
122 =VKPLTLSVHSERSQ=FPDFSVLTVTCTVNAFPHPHVQWLMPEG=VE=PAP=TAANGGVM 176
      .           140          .           160          .           180
301 RGKKLVQASASGVAQSKEPTTPKAKSVSAHLKSIFCEELLNKRVA* 346
      + K   + A   ++ K   P       +       +       *
177 KEKDGSLSAVDLSLPKPWHLPVTCVGKNDKEEAHGVYVSGYLSQ* 222
      180           .           200           .           220

```

% Identity = 9.5 (33/346) % Homology = 5.5 (19/346) % Total = 15.0 (52/346)

///

9310-13DVCTDV SEQ ID NO 5.xprt x Bankier et al. BA-RF1.xprt => Protein Alignment

Protein sequence 24 aa AVDTGSGGGGQP ... HDTAPRGARKKQ  
Protein sequence 222 aa MARFIAQLLLLA ... HGVIYVSGYLSQ\*

Method: Diagonals (BLOSUM62)      **Alignment 25.** Comparison of the amino acid sequence of  
Layout: Standard      SEQ ID NO:5 with the amino acid sequence, Ba-RF1, encoded  
Block Length ≤: 6-aa      by the nucleotide sequence of Fig. 2 of Bankier et al.  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

```
-----
1 MARFIAQLLLLLASCVAAGQAVTAFLGERVTLTSYWRRVSLGPEIEVSWFKLGPGEEQVLI 60
      .                20                .                40                .                60
-----

61 GRMHHDVIFIEWPFRGFFDIHRSANTFFLVVTAANISHDGNILCRMKLGETEVTKEHLS 120
      .                80                .                100                .                120
-----

121 VVKPLTSLVHSERSQFPDFSVLTVTCTVNAFPHPHVQWLMPEGVEPAPTAANGGVMKEKD 180
      .                140                .                160                .                180
      .                200                .                220
1 -----AVDTGSGGGGQPHDTAPRGARKKQ 24
      G      + H      G      +
181 GSLSVAVDLSLPKPWHLPVTCVGKNDKEEAHGVIYVSGYLSQ* 222
      .                200                .                220

% Identity = 1.4 (3/222)      % Homology = 0.9 (2/222)      % Total = 2.3 (5/222)
```

///

9310-13DVCTDV SEQ ID NO 6.xprt x Bankier et al. BA-RF1.xprt => Protein Alignment

Protein sequence 30 aa STAVAQSATPSV ... LRAATSGATAAA

Protein sequence 222 aa MARFIAQLLLLLA ... HGVIYVSGYLSQ\*

Method: Diagonals (BLOSUM62)  
 Layout: Standard  
 Block Length ≤: 6-aa  
 Mismatch penalty: Smaller (1)  
 Gap penalty: Medium (2)  
 Display: BLOSUM62

Alignment 26. Comparison of the amino acid sequence of  
 SEQ ID NO:6 with the amino acid sequence, Ba-RF1, encoded  
 by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .          20          .
1 STAV-AQSATPSVSSSISSLRAATSGATAAA----- 30
      AQ  +  +      A  G
1 MARFIAQLLLLLASCVAAGQAVTAFLGERVTLTSYWRRVSLGPEIEVSWFKLGPGEEQVLI 60
      .          20          .          40          .          60
-----
61 GRMHHDVIFIEWPFRGFFDIHRSANTFFLVVTAANISHDGNLYLCRMKLGETEVTKEHLS 120
      .          80          .          100          .          120
-----
121 VVKPLTSLVHSERSQFPDFSVLTVTCTVNAFPHPHVQWLMPEGVEPAPTAANGGVMKEKD 180
      .          140          .          160          .          180
-----
181 GSLSVAVDLSLPKPWHLPVTCVGKNDKEEAHGVIYVSGYLSQ* 222
      .          200          .          220
    
```

% Identity = 1.8 (4/222)      % Homology = 0.9 (2/222)      % Total = 2.7 (6/222)

///

9310-13DVCTDV SEQ ID NO 2.xprt x Bankier et al. BN-LF2a,b.xprt => Protein Alignment

Protein sequence 177 aa MARRLPKPTLQG ... DTAPRGARKKQ\*

Protein sequence 163 aa MVHVLERALLEQ ... LSLRCELGWCG\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 27.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:1 (SEQ ID NO:2) with the amino acid sequence, BN-LF2a,b, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .           20           .           40           .           60
1 MARRLPKPTLQGRLEADFPDSPLLPKFQELNQNNLPNDVVFREAQRSYLVFLTSQFCYEEY 60
  M  L +  L+ +  A                               P DV R  R  LV L  F
1 MVHVLERALLEQQSSACGLPGSSTETRPSHPCPEDP=DVSRL==RLLLVLVCVLFGLLCL 57
      .           20           .           40           .
61 VQRTFGVPRRQRAIDKRQRASVAGAGAHHLGGSSATPVQQAQAAASAGTGALASSAPST 120
  +           R  R +           +           + A           +           T  S
58 LLI*EATMRPGRPLAGFYATLRRSFRMSKRSKNKAKKERVVPVEDRPP=TPMPTSQRLIR 116
  60           .           80           .           100           .
121 AVAQSATPSVSSSISSLRAATSGATAAASAAAAVDTGSGGGGQPHDTAPRGARKKQ* 177
  A           +           R           S           D  S
117 RNALGGGVRPDAEDCIQRFHPLEPALGVSTKNF=DLLSLRCELGWCG*===== 163
  120           .           140           .           160           .

```

% Identity = 13.0 (23/177)      % Homology = 5.1 (9/177)      % Total = 18.1 (32/177)

///

9310-13DVCTDV SEQ ID NO 4.xprt x Bankier et al. BN-LF2a,b.xprt => Protein Alignment

Protein sequence 346 aa MLSGNAGEGATA ... FCELLNKRVA\*

Protein sequence 163 aa MVHVLERALLEQ ... LSLRCELGWCG\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 28.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:3 (SEQ ID NO:4) with the amino acid sequence, BN-LF2a,b, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .      .      20      .      40      .
1 MLSGNAGEGATACGGSAAAGQDLISVP-RNTFMTLLQTNLDNKPPRQTPLPYAAPLPPFS 59
  M+      E A      S+A G      S R +      ++      L      L
1 MVHVL==ERALLEQQSSACGLPGSSTETRPSPHPCPEDPDVSRRLRLLLVVLGVLFGLLCLL 58
      .      .      20      .      40      .
60 HQAIATAPSYGPGAGAVAPAGGYFTSPGGYYAGPAGGDPGAFLAMDAHTYHPHPHPPPAY 119
      AT      P AG A      F      A +      T P
59 LI*EATMRPGRPLAGFYATLRRSFRMSKRSKNKAKKERVVPVEDRPP=TPMPTSQRLIRR 117
60      .      80      .      100      .
120 FGLPGLFGPPPPCLLTDSHLRADYVPAPSRSNKRKRDPEDDEEGGGLFPGEDATLYRKD 179
      L G P      +      L      +      +      E G
118 NALGGGVRPDAEDCIQRFHPLEPALGVSTKNFDLLSLRCELGWCG*===== 163
120      .      140      .      160
180 IAGLSKSVNELQHTLQALRRRETLSYGHTGVGYCPQQGPCYTHSGPYGFQPHQSYEVPRYV 239
=====

240      .      260      .      280      .
240 PHPPPPPTSHQAAQAQPPPPGTQAPEAHCVAESTIPEAGAAGNSGPREDTNPQQPTTEGH 299
=====

300      .      320      .      340
300 HRGKKLVQASASGVAQSKEPTTPKAKSVSAHLKSIFCELLNKRVA* 346
=====

```

% Identity = 7.5 (26/347) % Homology = 2.6 (9/347) % Total = 10.1 (35/347)

///

9310-13DVCTDV SEQ ID NO 5.xprt x Bankier et al. BN-LF2a,b.xprt => Protein Alignment

Protein sequence 24 aa AVDTGSGGGGQP ... HDTAPRGARKKQ

Protein sequence 163 aa MVHVLERALLEQ ... LSLRCELGWCG\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 29.** Comparison of the amino acid sequence of SEQ ID NO:5 with the amino acid sequence, BN-LF2a,b, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .           20
1 AVDTGSGGGGQPHDTAPRGARKKQ----- 24
  V       +   +A
1 MVHVLERALLEQQSSACGLPGSSTETRPSHPCPEDPDVSRRLRLLLVVLCVLFGLLCLLLI 60
      .           20           .           40           .           60

-----

61 *EATMRPGRPLAGFYATLRRSFRMSKRSKNKAKKERVPVEDRPPTPMPTSQRLIRRNAL 120
      .           80           .           100           .           120

-----

121 GGGVRPDAEDCIQRFHPLEPALGVSTKNFDLLSLRCELGWCG* 163
      .           140           .           160

% Identity = 1.2 (2/163)      % Homology = 1.2 (2/163)      % Total = 2.5 (4/163)

```

///

9310-13DVCTDV SEQ ID NO 6.xprt x Bankier et al. BN-LF2a,b.xprt => Protein Alignment

Protein sequence 30 aa STAVAQSATPSV ... LRAATSGATAAA

Protein sequence 163 aa MVHVLERALLEQ ... LSLRCELGWCG\*

Method: Diagonals (BLOSUM62)  
 Layout: Standard  
 Block Length ≤: 6-aa  
 Mismatch penalty: Smaller (1)  
 Gap penalty: Medium (2)  
 Display: BLOSUM62

Alignment 30. Comparison of the amino acid sequence of  
 SEQ ID NO:6 with the amino acid sequence, BN-LF2a,b, encoded  
 by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .           20           .
1 STAVAQSATPSVSSSISSLRAATSGATAAA----- 30
      V + A      SS  L  +++  +
1 MVHVLERALLEQQSSACGLPGSSTETRPSPHPCPEDPDVSRRLRLLLVVLGVLFGLLCLLLI 60
      .           20           .           40           .           60
-----
61 *EATMRPGRPLAGFYATLRRSFRMSKRSKNKAKKERVPVEDRPPTPMPTSQRLIRRNAL 120
      .           80           .           100           .           120
-----
121 GGGVRPDAEDCIQRFHPLEPALGVSTKNFDLLSLRCELGWCG* 163
      .           140           .           160

```

% Identity = 3.1 (5/163)      % Homology = 3.1 (5/163)      % Total = 6.1 (10/163)

///



9310-13DVCTDV SEQ ID NO 2.xprt x Bankier et al. BN-LF1b.xprt => Protein Alignment

Protein sequence 177 aa MARRLPKPTLQG ... DTAPRGARKKQ\*

Protein sequence 269 aa VLGIWIYLLLEML ... PHGPVQLSYYD\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 31.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:1 (SEQ ID NO:2) with the amino acid sequence, BN-LF1b, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

-----
1 VLGIWIYLLLEMLWRLGATIWQLLAFFLAFFLDLILLIIALYLLQNNWWTLLVDLLWLLFL 60
      .                20                .                40                .                60
1 -----MARRLPKPTLQGRLEADFPDSPLLPKFQ 28
      .                .                .                .                .                .
61 AILIWMYYHGQRHSDEHHHDDSLPHPQQATDDSGHESDSNSNEGRHLLVSGAGDGPPLC 120
      .                .                .                .                .                .
      40                80                100                120
29 ELNQNNLPNDVFREARSYLVFLTSQFCYEEYVQRTFGVPRRQRAIDKRQRASVAGAGAH 88
      N                Q                +                P                Q                D
121 SQNLGAPGGGPDNGPQDPDNTDDNGPQDPDNTDDNGPHDPLPQ=DPDNTDDNGPQDPDNT 179
      .                .                .                .                .                .
      100                120                140                160
89 AHLGGSSATPVQQAQAAASAGTGALASSAPSTAVAQSATPSVSSSISSLRAATSGATAAA 148
      G                P                + +A + G G                +                P + +                + SG
180 DDNGPHDPLPHSPSDSAGNDG=GPPQLTEEEVENKGGDQGPPLMTDGGGGHSHDSGHGGGD 238
      180                .                200                .                220                .
      .                160                .
149 SAAAAVDTG-SGGGGQPHD-TAPRGARKKQ* 177
      + G SG GG D P                *
239 PHLPTLLLGSSSGSGGDDDDPHGPVQLSYYD* 269
      240                .                260

```

% Identity = 8.9 (24/271) % Homology = 4.4 (12/271) % Total = 13.3 (36/271)

///

9310-13DVCTDV SEQ ID NO 4.xprt x Bankier et al. BN-LF1b.xprt => Protein Alignment

Protein sequence 346 aa MLSGNAGEGATA ... FCEELLNKRVA\*

Protein sequence 269 aa VLGIWIYILLEML ... PHGPVQLSYD\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 32.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:3 (SEQ ID NO:4) with the amino acid sequence, BN-LF1b, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .           20           .           40           .           60
1  MLSGNAGEGATACGGSAAAGQDLISVPRNTFMTLLQTNLDNKPPRQTPLPYAAPLPFFSH 60
=====
      .           80           .           100          .           120
61 QAIATAPSYGPGAGAVAPAGGYFTSPGGYYAGPAGGDPGAFLAMDAHTYHPHPHPPPAYF 120
      V       Y       +   G       AF
1  =====VLGIWIY=LLEMLWRLGATIWQLLAFFLAFFLDLILLIIALYLYLQQ 44
      .           20           .           40
121 GLPGLFGPPPPCLLTDSHLRADYVPAPSRSNKRKRDPEDDEEGGGLFPGEDATLYRKDI 180
      L       LL   + L   Y       S++   D +
45 NWWTL=LVDLLWLLFLAILIWMYYHGQRHSDEHHHD=DSLPHPQQATDDSGHESDSNSN 102
      .           60           .           80           .           100
181 AGLSKSVNELQHTLQALRRETLSYGHTGVGYCPQQGPCYTHSGPYGFQPHQSYEVPRYVP 240
      G   +       L   + L       G       PQ       +GP       +P
103 EGRHLLVSGAGDGPPLCSQNLGAPGGGPDNGPQDPDNTDDNGPQDPDNTDDNGPHDPLP 162
      .           120          .           140          .           160
241 -HPPPPPTSHQAAQAQPPPPGTQAPEAHCVAESTIPEAGAAGNSGPREDTNPQQPTTEGH 299
      P   +       G       P   H   ++S   + G       +   E+       Q
163 QDPDNTDDNGPQDPDNTDDNGPHDPLPHSPSDSAGNDGGPPQLTEEVENKGGDQGPPLMT 222
      .           180          .           200          .           220
300 HRGKKLVQASASGVAQSKEPTTPKAKSVSAHLKSIFCEELLNKRVA* 346
      G       S   G       PT       S   S       +       *
223 DGGGGHSHDSGHGGGDPHLPTLLLGSSSGGDDDDPHGPVQLSYD* 269
      .           240          .           260

```

% Identity = 10.7 (37/347)      % Homology = 4.6 (16/347)      % Total = 15.3 (53/347)

///

9310-13DVCTDV SEQ ID NO 5.xprt x Bankier et al. BN-LF1b.xprt => Protein Alignment

Protein sequence 24 aa AVDTGSGGGGQP ... HDTAPRGARKKQ

Protein sequence 269 aa VLGIWIYLLLEML ... PHGPVQLSYD\*

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

Alignment 33. Comparison of the amino acid sequence of SEQ ID NO:5 with the amino acid sequence, BN-LF1b, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

-----
1 VLGIWIYLLLEMLWRLGATIWQLLAFFLAFFLDLILLIIALYLQQNWWTLLVDLLWLLLFL 60
      .                20                .                40                .                60
-----

61 AILIWMYYHGQRHSDEHHHDDSLPHPQQATDDSGHESDSNSNEGRHLLVSGAGDGPPLC 120
      .                80                .                100                .                120
-----

121 SQNLGAPGGGPDNGPQDPDNTDDNGPQDPDNTDDNGPHDPLPQDPDNTDDNGPQDPDNTD 180
      .                140                .                160                .                180
-----

181 DNGPHDPLPHSPSDSAGNDGGPPQLTEEEVENKGGDQGPPLMTDGGGGHSHDSGHGGGDPH 240
      .                200                .                220                .                240
      .                20
1 -----AVDTGSGGGGQP HDTAPRGARKKQ 24
      +GSGG                + +
241 LPTLLLGSSGSGGDDDDPHGPVQLSYD* 269
      .                260
-----

% Identity = 1.5 (4/269)      % Homology = 1.1 (3/269)      % Total = 2.6 (7/269)

```

///

9310-13DVCTDV SEQ ID NO 6.xprt x Bankier et al. BN-LF1b.xprt => Protein Alignment

Protein sequence 30 aa STAVAQSATPSV ... LRAATSGATAAA

Protein sequence 269 aa VLGIWIYILLEML ... PHGVPQLSYD\*

Method: Diagonals (BLOSUM62)  
 Layout: Standard  
 Block Length ≤: 6-aa  
 Mismatch penalty: Smaller (1)  
 Gap penalty: Medium (2)  
 Display: BLOSUM62

Alignment 34. Comparison of the amino acid sequence of  
 SEQ ID NO:6 with the amino acid sequence, BN-LF1b, encoded  
 by the nucleotide sequence of Fig. 2 of Bankier et al.

```

-----
1 VLGIWIYILLEMLWRLGATIWQLLAFFLAFFLDLILLIIALYLQQNWWTLLVDLLWLLLFL 60
      .                20                .                40                .                60
-----
61 AILIWMYYHGQRHSDEHHHDDSLPHPPQATDDSGHESDSNSNEGRHLLLVSGAGDGPPLC 120
      .                80                .                100                .                120
-----
121 SQNLGAPGGGPDNGPQDPDNTDDNGPQDPDNTDDNGPHDPLPQDPDNTDDNGPQDPDNTD 180
      .                140                .                160                .                180
1 -----ST 2
181 DNGPHDPLPHSPSDSAGNDGGPPQLTEEEVENKGGDQGPPPLMTDGGGGHSHDSGHGGGDPH 240
      .                200                .                220                .                240
      .                20                .
3 AVAQSATPSVS-SSISLRAATSGATAAA 30
      S S                +
241 LPTLLLGSSGSGGDDDDPHGVPQLSYD* 269
      .                260
% Identity = 0.7 (2/269)    % Homology = 0.4 (1/269)    % Total = 1.1 (3/269)
  
```

///

9310-13DVCTDV SEQ ID NO 2.xprt x Bankier et al. BN-LF1a.xprt => Protein Alignment

Protein sequence 177 aa MARRLPKPTLQG ... DTAPRGARKKQ\*

Protein sequence 144 aa MEHDLERGPPGP ... LGIVLFIFGCLL

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 35.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:1 (SEQ ID NO:2) with the amino acid sequence, BN-LF1a, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .           20           .           40           .           60
1  MARRLPKPTLQGRLEADFPDSPLLPKFQELNQNNLPNDVFREAQRSYLVFLTSQFCYEEY 60
   M  L  +      R      P      L      L      +      S      Y
1  MEHDLERGPPGPRRPPRGPPPLSSSLGLALLLLL=LALLFWLYIVMSDWTGGALLVLYSFA 59
      .           20           .           40           .
61 VQRTFGVPRRQRAIDKRQRASVAGAGAHHLGGSSATPVQQAQAAASAGTGALASSAPST 120
   +      +      I +R      GA      L      T      S+ + AL+ +P T
60 LMLIIIIILIIIF==IFRRDLLCPLGALCILLMSKYYTLCPTPPFPYSSFSNALSPSPVT 117
   60      .           80      .           100      .
      .           140      .           160      .
121 AVAQSATPSVSSSISSLRAATSGATAAASAAAAVDTGSGGGGQPHDTAPRGARKKQ* 177
   +      A  ++      L
118 LLLI=ALWNLHGQALFLGIVLFIFGCLL===== 144
   120      .           140

```

% Identity = 11.9 (21/177)      % Homology = 6.8 (12/177)      % Total = 18.6 (33/177)

///

9310-13DVCTDV SEQ ID NO 4.xprt x Bankier et al. BN-LF1a.xprt => Protein Alignment

Protein sequence 346 aa MLSGNAGEGATA ... FCEELLNKRVA\*

Protein sequence 144 aa MEHDLERGP PGP ... LGIVLFIFGCLL

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 36.** Comparison of the amino acid sequence encoded by the nucleotide sequence of SEQ ID NO:3 (SEQ ID NO:4) with the amino acid sequence, BN-LF1a, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .           20           .           40           .           60
1  MLSGNAGEGATACGGSAAAGQDLISVPRNTFMTLLQTNLDNKPPRQTPLPYAAPLPFFSH 60
  M      G      G      L      S      +      LL      L      +      A      L      +S
1  MEHDLER=GPPGPRRPPR=GPPLSSSLGLALLLLLLLALLFWLYIVMSDWTGGALLVLYSF 58
      .           20           .           40           .
61  QAIATAPSYGPGAGAVAPAGGYFTSPGGYYAGPAGGDPGAFLAMDAHTYHPHPHPPPAYF 120
  +
59  ALMLIIIIIIIFIFRRLDLCPLGALCILLMSKYYTLCPTPPFPYSSFSNALSPVTL 118
60      .           80           .           100           .
121 GLPGLFGPPPPCLLTDSHLRADYVPAPSRSNKRKRDPDEEDEEGGGLFPGEDATLYRKDI 180
  L      L+      L      +
119 LLIALWNLHGQALFLGIVLFIFGCLL===== 144
120      .           140           .           160           .           180
181 AGLSKSVNELQHTLQALRRETLSYGHTGVGYCPQQGPCYTHSGPYGFQPHQSYEVPRYVP 240
=====
      .           260           .           280           .           300
241 HPPPPPTSHQAAQAQPPPPGTQAPEAHCVAESTIPEAGAAGNSGPREDTNPQQPTTEGHH 300
=====
      .           320           .           340
301 RGKKLVQASASGVAQSKEPTTPKAKSVSAHLKSIFCEELLNKRVA* 346
=====

```

% Identity = 4.3 (15/346)      % Homology = 2.3 (8/346)      % Total = 6.6 (23/346)

///

9310-13DVCTDV SEQ ID NO 5.xprt x Bankier et al. BN-LF1a.xprt => Protein Alignment

Protein sequence 24 aa AVDTGSGGGGQP ... HDTAPRGARKKQ

Protein sequence 144 aa MEHDLERGPPGP ... LGIVLFIFGCLL

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

Alignment 37. Comparison of the amino acid sequence of  
SEQ ID NO:5 with the amino acid sequence, BN-LF1a, encoded  
by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .           20
1 AVDTGSGGGGQPHDTAPRGARKKQ----- 24
      G   P   PRG
1 MEHDLERGPPGP=PRGPPLSSSLGLALLLLLALLFWLYIVMSDWTGGALLVLYSFA 59
      .           20           .           40           .
-----
60 LMLIIIIIIIFIFRRDLLCPLGALCILLMSKYYTLCPTPPFPYSSFSNALSPVLTLL 119
60           .           80           .           100           .
-----
120 LIALWNLHGQALFLGIVLFIFGCLL 144
120           .           140
```

% Identity = 3.4 (5/145)      % Homology = 0.0 (0/145)      % Total = 3.4 (5/145)

///

9310-13DVCTDV SEQ ID NO 6.xprt x Bankier et al. BN-LF1a.xprt => Protein Alignment

Protein sequence 30 aa STAVAQSATPSV ... LRAATSGATAAA

Protein sequence 144 aa MEHDLERGPPGP ... LGIVLFIFGCLL

Method: Diagonals (BLOSUM62)  
Layout: Standard  
Block Length ≤: 6-aa  
Mismatch penalty: Smaller (1)  
Gap penalty: Medium (2)  
Display: BLOSUM62

**Alignment 38.** Comparison of the amino acid sequence of SEQ ID NO:6 with the amino acid sequence, BN-LF1a, encoded by the nucleotide sequence of Fig. 2 of Bankier et al.

```

      .           20           .
1 STAVAQSATPSVSSSISSLRAATSGATAAA----- 30
      +   P           ++S   A
1 MEHDLERGPPGPRRPPRGPPPLSSSLGLALLLLLLLALLFWLYIVMSDWTGGALLVLYSFAL 60
      .           20           .           40           .           60

-----

61 MLIIIIIIIIFIFRRDLLCPLGALCILLMSKYYTLCPTPPFPYSSFSNALSPVLTLL 120
      .           80           .           100           .           120

-----

121 IALWNLHGQALFLGIVLFIFGCLL 144
      .           140

```

% Identity = 2.1 (3/144)      % Homology = 2.1 (3/144)      % Total = 4.2 (6/144)

///